GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 14, 2000, 18:27:02 ; Search time 1381.26 Seconds
(without alignments)
-3066.588 Million cell updates/sec

Title: US-09-388-090-3
Perfect score: 1395
Sequence: 1 gtgttcaaaaaataccaata.....tcagggcaagtccccgtcaa 1395

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 821193 seqs, -1518192014 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1642386

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_pr1:*
10: gb_pr2:*
11: gb_pr3:*
12: gb_ro:*
13: gb_sts:*
14: gb_sy:*
15: gb_un:*
16: gb_vi:*
17: em_fun:*
18: em_hum1:*
19: em_hum2:*
20: em_in:*
21: em_om:*
22: em_or:*
23: em_ov:*
24: em_pat:*
25: em_ph:*
26: em_pl:*
27: em_ro:*
28: em_sts:*
29: em_sy:*
30: em_un:*
31: em_vi:*
32: gb_htg1:*
33: gb_htg2:*
34: gb_in1:*
35: gb_in2:*
36: em_ba1:*
37: em_ba2:*
38: em_hum3:*
39: em_hum4:*
40: gb_pr4:*
41: gb_htg3:*
42: gb_htg4:*
43: gb_htg5:*
44: gb_htg6:*
45: gb_htg7:*
46: em_htg1:*
47: em_htg2:*
48: em_htg3:*
49: em_hum5:*
50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	23	1.6	91	34	AG2H417	Z72082 A.gambiae s
c	2	23	1.6	93	34	AG2H442	Z72084 A.gambiae s
	3	20	1.4	1435	4	GGU72352	U72352 Gallus gall
	4	20	1.4	2890	1	GOGDH	X62710 G.oxydans g
c	5	20	1.4	31427	43	AC013843	AC013843 Drosophil
	6	20	1.4	144734	33	AC005052	AC005052 Homo sapi
	7	19	1.4	2153	10	HTLV1RES	X16660 Human HTLV-
c	8	19	1.4	4316	2	AF072440	AF072440 Enterobac
c	9	19	1.4	6417	12	AF067430	AF067430 Mus muscu
	10	19	1.4	36679	34	CELT14F9	U50199 Caenorhabdi
	11	19	1.4	38012	8	SPBC2F12	Z97211 S.pombe chr
c	12	19	1.4	60476	7	AB016875	AB016875 Arabidops
	13	19	1.4	93419	32	AC002415	AC002415 Homo sapi
c	14	18	1.3	247	12	MUSTHREX17	M62465 Mouse throm
c	15	18	1.3	400	13	G14673	G14673 human STS S
c	16	18	1.3	423	1	AB011872	AB011872 Unidentif
c	17	18	1.3	459	9	HSGATA3P	X73519 H.sapiens h
c	18	18	1.3	559	16	HSVRSAN	M24213 Herpesvirus
c	19	18	1.3	1474	34	GIU83277	U83277 Giardia int
c	20	18	1.3	1549	7	D78602	D78602 Arabidopsis
	21	18	1.3	1664	4	DRGROUCH1	Y12467 D.rerio mRN
	22	18	1.3	1664	4	DRU96451	U96451 Danio rerio
c	23	18	1.3	1796	12	AF087654	AF087654 Mus muscu
c	24	18	1.3	1861	35	TCU14732	U14732 Tribolium c
	25	18	1.3	2543	35	AF188715	AF188715 Caenorhab
	26	18	1.3	2809	10	HSU67369	U67369 Human growt
c	27	18	1.3	3537	4	CHKTHBSA	M60853 Chicken thr
c	28	18	1.3	4339	12	MUSTSP1A	M87276 Mouse throm
	29	18	1.3	4373	1	MISPT	X95538 M.intracell
c	30	18	1.3	6194	41	AC008595	AC008595 Homo sapi
	31	18	1.3	7744	1	HIFIMGC	Z33502 H.influenza
c	32	18	1.3	9513	1	TAA224959	AJ224959 Thauera a
	33	18	1.3	10249	2	MTU68480	U68480 Mycobacteri
	34	18	1.3	11684	2	AE000263	AE000263 Escherich
c	35	18	1.3	11904	2	PAU79580	U79580 Pseudomonas
c	36	18	1.3	12360	43	AC015011	AC015011 Drosophil
	37	18	1.3	15131	2	AE000729	AE000729 Aquifex a
	38	18	1.3	16951	2	MSU46844	U46844 Mycobacteri
c	39	18	1.3	19521	1	D90811	D90811 E.coli geno
c	40	18	1.3	28611	34	CEC02D4	Z81031 Caenorhabdi
c	41	18	1.3	34305	34	CEW02B12	Z66521 Caenorhabdi
c	42	18	1.3	34983	2	SCM11	AL133278 Streptomy
c	43	18	1.3	37005	11	AC005239	AC005239 Homo sapi
	44	18	1.3	37085	1	MTY13D12	Z80343 Mycobacteri
	45	18	1.3	37164	1	MSGY126	AD000012 Mycobacte
	46	18	1.3	38017	10	AC000396	AC000396 Genomic s
c	47	18	1.3	39951	11	AC005602	AC005602 Homo sapi
c	48	18	1.3	40075	34	CET28D6	Z81134 Caenorhabdi
	49	18	1.3	41171	1	U00010	U00010 Mycobacteri
c	50	18	1.3	44189	41	AC011540	AC011540 Homo sapi
	51	18	1.3	45097	35	CELB0416	U23516 Caenorhabdi
c	52	18	1.3	46632	41	AC009588	AC009588 Homo sapi
	53	18	1.3	54225	46	AC006090	Ac006090 *** SEQUE
	54	18	1.3	55028	40	AC016473	AC016473 Homo sapi
	55	18	1.3	56686	44	AC016415	AC016415 Homo sapi
c	56	18	1.3	67220	45	AC017014_3	Continuation (4 of

	57	18	1.3	73009	8	ATAC007069 AC007069 Arabidops
	58	18	1.3	74901	35	AC005474 AC005474 Drosophil
	59	18	1.3	83859	7	AB024038 AB024038 Arabidops
c	60	18	1.3	100793	11	AF070717 AF070717 Homo sapi
	61	18	1.3	120391	45	AC017146 AC017146 Drosophil
	62	18	1.3	124469	41	AC008347 AC008347 Drosophil
c	63	18	1.3	129441	32	HSAC002099 AC002099 Homo sapi
c	64	18	1.3	132353	33	AC002355 AC002355 Homo sapi
	65	18	1.3	137658	10	HS1022J11 AL049765 Human DNA
	66	18	1.3	152355	11	AC005668 AC005668 Homo sapi
	67	18	1.3	156187	44	AC013593 AC013593 Homo sapi
	68	18	1.3	157066	42	AC010436 AC010436 Homo sapi
	69	18	1.3	160437	43	AC011984 AC011984 Homo sapi
	70	18	1.3	166942	10	HS1054A22 AL031651 Human DNA
	71	18	1.3	168571	11	CNS01DUF AL133249 BAC seque
	72	18	1.3	168835	11	HS652L8 AL031734 Human DNA
c	73	18	1.3	176865	42	AC008525 AC008525 Homo sapi
c	74	18	1.3	177726	11	AC004083 AC004083 Homo sapi
	75	18	1.3	178328	44	AC007299 AC007299 Drosophil
	76	18	1.3	183007	35	AC007257 AC007257 Drosophil
c	77	18	1.3	185116	11	AC005823 AC005823 Homo sapi
c	78	18	1.3	202540	11	AC002524 AC002524 Homo sapi
	79	18	1.3	210296	33	HS1057B20 AL109823 Homo sapi
	80	18	1.3	212118	43	AC009264 AC009264 Homo sapi
c	81	18	1.3	310565	32	CEY62F5 AL023633 Caenorhab
c	82	18	1.3	330250	40	AF049895 AF049895 Homo sapi
c	83	18	1.3	337565	32	CEY47D3 Z98865 Caenorhabdi
	84	17	1.2	129	8	AF099426 AF099426 Zea mays
	85	17	1.2	135	12	MMU133878 AJ133878 Mus muscu
c	86	17	1.2	354	9	HS303C10 Z79883 H.sapiens c
	87	17	1.2	359	13	G45126 G45126 Z17274_1 Ze
	88	17	1.2	528	4	MTPS16SR X99173 Petrocephal
	89	17	1.2	548	4	PBU33533 U33533 Petrocephal
	90	17	1.2	804	16	ROTIDIR9 D00911 IDIR agent
c	91	17	1.2	898	7	HEVER1PS M88255 Hevea brasi
	92	17	1.2	1005	3	DOGBGALL L23429 Canis beta-
c	93	17	1.2	1012	9	HS19PT009 Z96436 H.sapiens t
c	94	17	1.2	1029	7	CALIPASB Z30645 C.antarctic
	95	17	1.2	1080	1	FPLTRAU M34695 F plasmid (
c	96	17	1.2	1195	1	BLTHYBL Z50165 B.lichenifo
c	97	17	1.2	1220	8	AF079296 AF079296 Melica cu
	98	17	1.2	1510	12	AB00515S42 AB005191 Mus muscu
	99	17	1.2	1597	40	AF020760 AF020760 Homo sapi
	100	17	1.2	1620	4	GGVITRO Y11030 G.gallus mR
	101	17	1.2	1621	12	AF175324 AF175324 Mus muscu
	102	17	1.2	1705	3	BOVUROPLAK L19542 Bovine urop
c	103	17	1.2	1769	10	HSM801100 AL117412 Homo sapi
c	104	17	1.2	1864	9	HUMELF4AII D30655 Homo sapien
c	105	17	1.2	1872	16	BIMSEPC L43129 Bovine immu
c	106	17	1.2	1881	10	S79942 S79942 EIF4A2=prot
c	107	17	1.2	1925	7	CEZ98952 Z98952 Calymperes
c	108	17	1.2	1933	7	DSZ98956 Z98956 Dicranum sc
	109	17	1.2	1938	4	GGU72394 U72394 Gallus gall
c	110	17	1.2	2757	8	AF042275 AF042275 Oryza sat
c	111	17	1.2	2758	7	SCYKR024C Z28249 S.cerevisia
c	112	17	1.2	2882	9	HSMUC181 X68264 H.sapiens M
c	113	17	1.2	3263	35	AF010326 AF010326 Drosophil
	114	17	1.2	3276	12	RNTFNF1A X84210 R.norvegicu
c	115	17	1.2	3283	35	AF010328 AF010328 Drosophil
c	116	17	1.2	3286	35	AF010327 AF010327 Drosophil
c	117	17	1.2	3291	35	AF010325 AF010325 Drosophil
	118	17	1.2	3368	12	RNTFNF1 X84209 R.norvegicu
c	119	17	1.2	3450	1	XCAJ2070 AJ002070 Xanthomon
c	120	17	1.2	3691	7	D87895 D87895 Aspergillus
	121	17	1.2	3864	40	AF096300 AF096300 Homo sapi
	122	17	1.2	3970	35	AF114486 AF114486 Drosophil
	123	17	1.2	4064	9	HSU09607 U09607 Human JAK f
	124	17	1.2	4266	9	AB014587 AB014587 Homo sapi
c	125	17	1.2	4794	2	AF055586 AF055586 Vibrio ch
	126	17	1.2	4864	9	HSCMRP X96395 H.sapiens m
c	127	17	1.2	4968	16	SH1SEQ M81222 Herpesvirus
c	128	17	1.2	5341	11	HSSMAD2S1 U78726 Homo sapien
c	129	17	1.2	5896	1	PDQOXABCD X78196 P.denitrifi
c	130	17	1.2	5907	1	ECSAPABCD X97282 E.coli sapA
	131	17	1.2	6057	1	AB014757 AB014757 Pseudomon
c	132	17	1.2	6191	2	RPU75364 U75364 Rhodopseudo
	133	17	1.2	6597	9	HSCAN X64228 H.sapiens c
	134	17	1.2	6642	9	HUMORF10 D14689 Human mRNA
c	135	17	1.2	6682	2	AF170704 AF170704 Streptomy
c	136	17	1.2	6738	2	AF116907 AF116907 Rhodococc
	137	17	1.2	6824	6	AF112470 AF112470 Streptoco
	138	17	1.2	8757	4	AB018707S4 AB018710 Gallus ga
	139	17	1.2	10477	2	AE000227 AE000227 Escherich
	140	17	1.2	11342	1	AF005044 AF005044 Escherich
	141	17	1.2	11344	40	AF034611 AF034611 Homo sapi
c	142	17	1.2	11978	2	AE001955 AE001955 Deinococc
	143	17	1.2	12298	16	AF092448 AF092448 Hog chole
	144	17	1.2	12437	12	AB007544 AB007544 Mus muscu
	145	17	1.2	12457	12	AB011543 AB011543 Mus muscu
	146	17	1.2	12653	12	D87521 D87521 Mus musculu
	147	17	1.2	13857	2	AE000185 AE000185 Escherich
	148	17	1.2	15009	43	AC014599 AC014599 Drosophil
	149	17	1.2	15141	16	SH1PROIE M34651 Pseudorabie
	150	17	1.2	15231	12	RNPLECT X59601 Rat mRNA fo
	151	17	1.2	16578	1	D90721 D90721 Escherichia
	152	17	1.2	17769	1	D90767 D90767 E.coli geno
	153	17	1.2	18399	41	AC010652 AC010652 Homo sapi
	154	17	1.2	19196	1	D90768 D90768 E.coli geno
c	155	17	1.2	20252	2	AF029714 AF029714 Pseudomon
c	156	17	1.2	22449	1	SPSNBCDE Y11548 S.pristinae
c	157	17	1.2	22449	1	SPSNBCGEN X98690 S.pristinae
c	158	17	1.2	24754	41	AC008674 AC008674 Homo sapi
c	159	17	1.2	25420	34	CELK08F11 U70855 Caenorhabdi
c	160	17	1.2	28762	34	CEZC376 Z77136 Caenorhabdi
	161	17	1.2	30000	16	BHV130KB Z48053 Bovine herp
	162	17	1.2	30352	1	MTCY409 Z97188 Mycobacteri
c	163	17	1.2	31896	45	AC017879 AC017879 Drosophil
c	164	17	1.2	32591	34	CEF16D3 Z78062 Caenorhabdi
	165	17	1.2	33359	2	U01159 U01159 Escherichia
	166	17	1.2	33384	41	AC008915 AC008915 Homo sapi
c	167	17	1.2	34584	34	CET27C5 Z82058 Caenorhabdi
c	168	17	1.2	34872	41	AC010408 AC010408 Homo sapi
c	169	17	1.2	34877	43	AC013124 AC013124 Drosophil
c	170	17	1.2	35637	7	SPCC74 AL031543 S.pombe c
c	171	17	1.2	37881	34	CELK09H9 AF043700 Caenorhab
	172	17	1.2	40739	6	AF115103 AF115103 Streptoco
	173	17	1.2	41052	11	AC002499 AC002499 Human Cos
	174	17	1.2	41055	1	SC6G4 AL031317 Streptomy
	175	17	1.2	41084	10	AC002500 AC002500 Human Cos
c	176	17	1.2	41321	1	MSGY409 AD000017 Mycobacte
	177	17	1.2	41552	34	CEC17D12 Z81473 Caenorhabdi
c	178	17	1.2	41716	43	AC014073 AC014073 Drosophil
c	179	17	1.2	42800	41	AC010288 AC010288 Homo sapi
c	180	17	1.2	43802	34	CEK07F5 Z70284 Caenorhabdi
c	181	17	1.2	44993	43	AC014424 AC014424 Drosophil
c	182	17	1.2	49377	5	I88042 I88042 Sequence 1
c	183	17	1.2	50714	35	AC005471 AC005471 Drosophil
	184	17	1.2	52298	42	AC012403 AC012403 Homo sapi
	185	17	1.2	52359	41	AC010772 AC010772 Homo sapi
	186	17	1.2	53517	32	AC002405 AC002405 Homo sapi
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c	188	17	1.2	66489	44	AC016267 AC016267 Homo sapi
c	189	17	1.2	67747	42	AC012630 AC012630 Homo sapi
c	190	17	1.2	70932	10	AP000269 AP000269 Homo sapi
c	191	17	1.2	77118	43	AC015954 AC015954 Homo sapi
	192	17	1.2	77201	45	AC007307 AC007307 Mus muscu
	193	17	1.2	78583	41	AC009709 AC009709 Homo sapi
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	195	17	1.2	80470	44	AC015678 AC015678 Homo sapi
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	199	17	1.2	83083	44	AC013671 AC013671 Homo sapi
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	201	17	1.2	85420	40	AC004672 AC004672 Homo sapi
	202	17	1.2	85943	41	AC009472 AC009472 Homo sapi

203	17	1.2	86212	7	AB010074
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c 207	17	1.2	89765	45	AC017970
208	17	1.2	91019	35	AC001658
c 209	17	1.2	91421	33	AC008105
210	17	1.2	93216	11	AC003016
211	17	1.2	94281	1	AP000342
c 212	17	1.2	96964	33	AC004906
213	17	1.2	97487	41	AC011433
214	17	1.2	97542	43	AF202964
c 215	17	1.2	97854	45	AC017411
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c 218	17	1.2	100000	10	AP000103
c 219	17	1.2	100000	10	AP000179
c 220	17	1.2	100666	32	CEY20C6
221	17	1.2	105325	11	HS614C15
222	17	1.2	105607	43	AC013410
c 223	17	1.2	106926	40	AF042089
224	17	1.2	109016	8	ATT10K17
225	17	1.2	110000	32	CEY47H9_1
226	17	1.2	111390	8	AC000348
227	17	1.2	116215	11	AC004130
228	17	1.2	116490	32	HSJ189K14
229	17	1.2	120206	11	HS439F8
230	17	1.2	121121	41	AC010580
231	17	1.2	121474	41	AC007150
c 232	17	1.2	123872	33	AC008209
233	17	1.2	125032	40	AC007099
234	17	1.2	125237	33	AC008186
c 235	17	1.2	126534	41	AC008750
c 236	17	1.2	126813	41	AF165423
c 237	17	1.2	127596	42	AF165177
238	17	1.2	128230	11	HS313L4
239	17	1.2	134365	41	AC006519
240	17	1.2	135301	16	BHV1CGEN
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242	17	1.2	138445	33	AC002979
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c 246	17	1.2	146174	1	D90910
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264	17	1.2	163869	43	AC013276
265	17	1.2	164655	40	AC007687
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268	17	1.2	166888	33	AC007608
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c 270	17	1.2	171788	43	AC011170
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AB010074 Arabidops
AC017906 Drosophil
AC007454 Arabidops
AC006577 Sequence
AC017970 Drosophil
AC001658 Drosophil
AC008105 Homo sapi
AC003016 Human BAC
AP000342 Plasmid R
AC004906 Homo sapi
AC011433 Homo sapi
AF202964 Homo sapi
AC017411 Drosophil
AF188025 Homo sapi
AP000032 Homo sapi
AP000103 Homo sapi
AP000179 Homo sapi
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AL035250 Human DNA
AC013410 Homo sapi
AF042089 Homo sapi
AL132977 Arabidops
Continuation (2 of
AC000348 Genomic s
AC004130 Homo sapi
AL121966 Homo sapi
AL021392 Human DNA
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AC007150 Drosophil
AC008209 Drosophil
AC007099 Homo sapi
AC008186 Drosophil
AC008750 Homo sapi
AF165423 Homo sapi
AF165177 Homo sapi
Z99943 Human DNA s
AC006519 Homo sapi
AJ004801 Bovine he
AC011138 Homo sapi
AC002979 Homo sapi
AC006302 Drosophil
AC015869 Homo sapi
AL022724 Human DNA
D90910 Synechocyst
AC012284 Homo sapi
AC004642 Drosophil
AC004695 Homo sapi
AC011510 Homo sapi
Z99496 Human DNA s
AL121796 Homo sapi
AC007653 Homo sapi
AL078630 Mus muscu
Z97987 Human DNA s
AC007413 Drosophil
AC006472 Drosophil
AC013270 Homo sapi
AC005534 Homo sapi
AC011606 Homo sapi
AC011432 Homo sapi
AC007911 Homo sapi
AC015821 Homo sapi
AC013276 Homo sapi
AC007687 Homo sapi
AL033525 Human DNA
AC013394 Homo sapi
AC007608 Homo sapi
AC007404 Homo sapi
AC011170 Homo sapi
AC002324 Mus muscu
AC006247 Drosophil
AL035089 Homo sapi
AC009863 Homo sapi
AC005805 Homo sapi

c 276	17	1.2	177316	41	AC009456
277	17	1.2	179482	32	HSDJ92C4
278	17	1.2	181564	44	AC010977
c 279	17	1.2	183687	41	AC010739
c 280	17	1.2	184457	2	AF079317
281	17	1.2	185792	44	AC011028
282	17	1.2	186494	33	AL133323
c 283	17	1.2	186557	42	AC011191
c 284	17	1.2	187886	42	AC011851
285	17	1.2	190014	7	AP000836
c 286	17	1.2	190528	42	AC010729
c 287	17	1.2	191356	40	AC005041
c 288	17	1.2	192823	43	AC012149
c 289	17	1.2	193708	40	AC005035
290	17	1.2	195257	33	AC008177
c 291	17	1.2	195364	11	HS431A14
c 292	17	1.2	196337	35	AC005894
c 293	17	1.2	198303	45	AC013285
294	17	1.2	202291	44	AC007147
295	17	1.2	202860	8	ATFCA2
296	17	1.2	207674	8	ATFCA8
c 297	17	1.2	209365	33	AC006719
c 298	17	1.2	212870	44	AC010203
299	17	1.2	213721	10	HS172B20
300	17	1.2	213732	2	AE001862
301	17	1.2	217495	42	AC012613
302	17	1.2	218470	1	BSUB0013
303	17	1.2	230278	16	MCU68299
304	17	1.2	233053	33	HSDJ920G3
305	17	1.2	234523	40	AC006544
306	17	1.2	246546	40	AF152365
c 307	17	1.2	253073	46	AC010171
c 308	17	1.2	254877	33	AC006904
309	17	1.2	270405	33	HSB258O15
c 310	17	1.2	282700	1	BACJH642
c 311	17	1.2	292390	33	AC006900
c 312	17	1.2	303319	42	AC006927
c 313	17	1.2	306131	33	AC006874
314	17	1.2	337101	10	HSXKSRPXR
c 315	17	1.2	348116	41	AC010138
316	16	1.1	179	1	ECOGYRBA
c 317	16	1.1	195	9	HS13H6R
c 318	16	1.1	245	8	AF013303
c 319	16	1.1	249	8	AF058853
c 320	16	1.1	256	40	AF121405
321	16	1.1	279	8	AF184830
c 322	16	1.1	301	4	XELCRLB
c 323	16	1.1	312	16	AF041112
c 324	16	1.1	336	12	MMU55393
c 325	16	1.1	374	13	AU029126
326	16	1.1	382	5	I09073
c 327	16	1.1	386	13	G01682
c 328	16	1.1	387	13	G11729
c 329	16	1.1	388	5	I22429
330	16	1.1	388	13	G50046
331	16	1.1	452	35	AF193256
332	16	1.1	455	9	HSALL1X1
c 333	16	1.1	465	3	BTU51932
c 334	16	1.1	467	4	XELCRLD
335	16	1.1	472	13	HSPE46B12
c 336	16	1.1	479	7	AB025003
c 337	16	1.1	483	4	XELCRLJ
c 338	16	1.1	493	16	BIU80944
339	16	1.1	577	35	AF169218
340	16	1.1	608	3	BTCNP2
341	16	1.1	685	35	AF107488
342	16	1.1	686	34	AB005583
c 343	16	1.1	701	4	XELCRLG
c 344	16	1.1	820	1	BSDAT1
345	16	1.1	839	16	PRU14741
346	16	1.1	839	16	PRU14743
c 347	16	1.1	888	2	PSEOPRFE
c 348	16	1.1	894	24	E11868

AC009456 Homo sapi
AL132875 Homo sapi
AC010977 Homo sapi
AC010739 Homo sapi
AF079317 Sphingomo
AC011028 Homo sapi
AL133323 Homo sapi
AC011191 Homo sapi
AC011851 Homo sapi
AP000836 Oryza sat
AC010729 Homo sapi
AC005041 Homo sapi
AC012149 Homo sapi
AC005035 Homo sapi
AC008177 Homo sapi
Z85996 Human DNA s
AC005894 Drosophil
AC013285 Homo sapi
AC007147 Drosophil
Z97337 Arabidopsis
Z97343 Arabidopsis
AC006719 Caenorhab
AC010203 Homo sapi
AL022319 Human DNA
AE001862 Deinococc
AC012613 Homo sapi
Z99116 Bacillus su
U68299 Mouse cytom
AL121995 Homo sapi
AC006544 , complet
AF152365 Homo sapi
Ac010171 Homo sapi
AC006904 Caenorhab
AL121871 Homo sapi
D84432 Bacillus su
AC006900 Caenorhab
AC006927 Homo sapi
AC006874 Caenorhab
AL121578 Homo sapi
AC010138 Homo sapi
M15548 E.coli gyrB
Z59279 H.sapiens C
AF013303 Bryonia c
AF058853 Centaurea
AF121405 Homo sapi
AF184830 Arabidops
K00930 Xenopus lae
AF041112 HIV-1 iso
U55393 Mus musculu
AU029126 Rattus no
I09073 Sequence 1
G01682 chicken STS
G11729 human STS W
I22429 Sequence 10
G50046 SHGC-79745
AF193256 Conus pen
Z69744 H.sapiens A
U51932 Bos taurus
M12493 X.laevis pr
AL010033 H.sapiens
AB025003 Cicer ari
M12454 X.laevis ca
U80944 Bovine immu
AF169218 Loligo pe
Z48478 B.taurus mR
AF107488 Coptoterm
AB005583 Coptoterm
M12304 X.laevis pr
X15659 Bacillus su
U14741 Papaya ring
U14743 Papaya ring
L21199 Pseudomonas
E11868 Mutated DNA

	349	16	1.1	918	24	E11731 E11731 cDNA encodi
c	350	16	1.1	951	1	PFU19743 U19743 Pseudomonas
c	351	16	1.1	951	1	PSEOPRFH L21202 Pseudomonas
c	352	16	1.1	962	2	AF117965 AF117965 Pseudomon
c	353	16	1.1	973	16	AF102782 AF102782 Banana bu
c	354	16	1.1	981	2	AF117969 AF117969 Pseudomon
	355	16	1.1	1000	7	LETFT5 X95903 L.esculentu
	356	16	1.1	1004	3	BTCNP1 Z48477 B.taurus mR
c	357	16	1.1	1018	12	RATCPSI13 M12335 Rat nucleus
	358	16	1.1	1041	2	AF044794 AF044794 Neisseria
	359	16	1.1	1047	2	AF090797 AF090797 Neisseria
c	360	16	1.1	1054	2	BCY15704 Y15704 Bacillus ci
c	361	16	1.1	1065	10	AF007782 AF007782 Homo sapi
	362	16	1.1	1071	1	NGU75635 U75635 Neisseria g
	363	16	1.1	1071	1	NGU75636 U75636 Neisseria g
c	364	16	1.1	1075	8	SST242803 AJ242803 Sporobolu
	365	16	1.1	1103	12	D78265 D78265 Mus musculu
c	366	16	1.1	1105	9	HSSYN2GEN X89851 H.sapiens D
c	367	16	1.1	1122	1	STLEUB X53376 S.typhimuri
	368	16	1.1	1125	16	PAYCP D50591 Papaya ring
c	369	16	1.1	1126	12	RNCPSIX38 Z27513 R.norvegicu
	370	16	1.1	1148	5	E12704 E12704 Papaya ring
c	371	16	1.1	1151	7	PCU17117 U17117 Pneumocysti
	372	16	1.1	1152	34	AB010284 AB010284 Trypanoso
	373	16	1.1	1279	4	AB022691 AB022691 Xenopus l
	374	16	1.1	1287	12	MUSCYPC M74227 Mouse cyclo
c	375	16	1.1	1288	4	XLEIF4AI Y12590 X.laevis mR
	376	16	1.1	1288	5	I14303 I14303 Sequence 4
c	377	16	1.1	1300	1	STU20795 U20795 Salmonella
	378	16	1.1	1320	2	RMU51475 U51475 Rhizobium m
	379	16	1.1	1348	1	ESU13036 U13036 Eubacterium
	380	16	1.1	1351	16	AF120270 AF120270 Papaya ri
	381	16	1.1	1357	35	MSU11879 U11879 Manduca sex
	382	16	1.1	1364	34	MOTP4A M64346 Manduca sex
	383	16	1.1	1375	1	PEP16SRR19 D14154 Peptostrept
	384	16	1.1	1401	1	ESRIBRNA1 Z36271 Eubacterium
c	385	16	1.1	1401	35	CPU43545 U43545 Culex pipie
c	386	16	1.1	1421	34	MSLMTFR6A M83761 Mytilus edu
c	387	16	1.1	1436	6	P29P3P4 J02479 Bacteriopha
	388	16	1.1	1440	4	SSAJ664 AJ000664 Salmo sal
	389	16	1.1	1475	2	SEU43309 U43309 Salmonella
	390	16	1.1	1476	1	PSU33313 U33313 Pseudomonas
c	391	16	1.1	1479	1	DNEPS3PS Z29339 D.nodosus (
c	392	16	1.1	1479	5	AR038196 AR038196 Sequence
c	393	16	1.1	1479	5	I44026 I44026 Sequence 68
c	394	16	1.1	1479	5	I49035 I49035 Sequence 68
	395	16	1.1	1480	4	SSAJ665 AJ000665 Salmo sal
	396	16	1.1	1533	35	AF132170 AF132170 Drosophil
	397	16	1.1	1534	34	TCSBTUB L23506 Trichostron
	398	16	1.1	1542	7	CROEE3 X13832 C.reinhardt
c	399	16	1.1	1561	16	U87663 U87663 Hepatitis G
c	400	16	1.1	1600	4	XLEIF4AII Y12591 X.laevis mR
c	401	16	1.1	1601	35	AF092910 AF092910 Trypanoso
	402	16	1.1	1620	40	HUMS6KINB L07598 Homo sapien
c	403	16	1.1	1656	7	BLYRCAB M55448 Hordeum vul
	404	16	1.1	1662	12	CPO238589 AJ238589 Cavia por
c	405	16	1.1	1674	34	DROSLITEGF M23543 Drosophila
	406	16	1.1	1679	4	AF001299 AF001299 Danio rer
	407	16	1.1	1694	34	BMJ000916 AJ000916 Brugia ma
c	408	16	1.1	1695	1	MSGY414B AD000011 Mycobacte
c	409	16	1.1	1720	12	RNU55276 U55276 Rattus norv
	410	16	1.1	1722	16	LCVY16308 Y16308 Lymphocytic
c	411	16	1.1	1728	9	HUMHPSA D61391 Human mRNA
c	412	16	1.1	1738	3	AF076281 AF076281 Mustela v
c	413	16	1.1	1758	1	PAAMPC X54719 P. aerugino
	414	16	1.1	1760	16	AF063220 AF063220 Papaya ri
	415	16	1.1	1763	16	AF063221 AF063221 Papaya ri
	416	16	1.1	1791	34	AB013012 AB013012 Doliolum
c	417	16	1.1	1811	1	STPEPMG X55778 S. typhimur
c	418	16	1.1	1840	2	XANPELY L38573 Xanthomonas
c	419	16	1.1	1845	35	AF099185 AF099185 Drosophil
	420	16	1.1	1857	1	D89826 D89826 Escherichia
c	421	16	1.1	1871	12	MMU36274 U36274 Mus musculu
c	422	16	1.1	1930	7	CPZ98955 Z98955 Ceratodon p
c	423	16	1.1	1933	7	SAZ98958 Z98958 Schistidium
	424	16	1.1	1958	1	PSESEQB L07613 Pseudomonas
c	425	16	1.1	1968	7	PTZ98957 Z98957 Pottia trun
	426	16	1.1	1983	35	AF181634 AF181634 Drosophil
	427	16	1.1	2004	1	STAQACD M37888 Staphylococ
c	428	16	1.1	2026	4	GGU47276 U47276 Gallus gall
	429	16	1.1	2038	1	ECXERB X15130 E. coli xer
	430	16	1.1	2061	5	E08061 E08061 DNA encodin
	431	16	1.1	2061	5	I23834 I23834 Sequence 9
	432	16	1.1	2061	5	I43345 I43345 Sequence 5
	433	16	1.1	2061	5	I44694 I44694 Sequence 5
	434	16	1.1	2076	35	AF188888 AF188888 Musca dom
	435	16	1.1	2090	1	PAU17232 U17232 Pseudomonas
	436	16	1.1	2107	34	DDIADCYA03 L05498 Dictyosteli
	437	16	1.1	2108	9	D50914 D50914 Human mRNA
	438	16	1.1	2130	11	AF078107 AF078107 Homo sapi
	439	16	1.1	2157	5	AR054117 AR054117 Sequence
	440	16	1.1	2157	9	HSRRMRNA X59155 H.sapiens r
	441	16	1.1	2161	9	HSREC1L X57303 H.sapiens R
	442	16	1.1	2169	12	MMU132236 AJ132236 Mus muscu
c	443	16	1.1	2195	1	ECOEXBBD M28819 E.coli exbB
c	444	16	1.1	2224	34	DME243607 AJ243607 Drosophil
	445	16	1.1	2232	1	ECPEPCAR X86443 E.coli pepA
	446	16	1.1	2415	1	D87842 D87842 Escherichia
	447	16	1.1	2415	1	STGYRB Y07916 S.typhimuri
	448	16	1.1	2415	1	STGYRBQR Y08383 S.typhimuri
	449	16	1.1	2472	2	NMU79481 U79481 Neisseria m
	450	16	1.1	2502	1	BACCDG M12777 B.mecerans
	451	16	1.1	2508	12	RNUDPNAGE Y07744 R.norvegicu
	452	16	1.1	2512	12	D78264 D78264 Mus musculu
c	453	16	1.1	2552	34	DME243599 AJ243599 Drosophil
	454	16	1.1	2631	1	BMCGTM X59045 B.macerans
c	455	16	1.1	2670	1	CECEQI Z34099 C.equii DNA
	456	16	1.1	2683	1	BAJ10128 AJ010128 Bacillus
	457	16	1.1	2692	16	PRVNIBCTP X96538 Papaya ring
	458	16	1.1	2765	34	CBU45326 U45326 Caenorhabdi
c	459	16	1.1	2781	34	S81337 S81337 18S rRNA [A
	460	16	1.1	2791	9	HSRNARS6K X85106 H.sapiens m
	461	16	1.1	2798	1	XCPROTEA X51635 X.campestri
	462	16	1.1	2808	7	RICPRKI L27821 Oryza sativ
c	463	16	1.1	2812	1	ECOSNGLPD M55989 E.coli sn-g
	464	16	1.1	2831	1	SSQACFREP Z37964 Staphylococ
c	465	16	1.1	2838	1	ECOGLPDA D00425 E. coli glp
c	466	16	1.1	2847	12	CGPRU28A X79298 C.griseus r
c	467	16	1.1	2936	1	ECPBPA X04516 E. coli pbp
c	468	16	1.1	2940	8	AF180367 AF180367 Aspergill
	469	16	1.1	2960	16	PRVNIAB X78557 Papaya ring
	470	16	1.1	2962	8	CRU73856 U73856 Chlamydomon
	471	16	1.1	3025	2	AF047363 AF047363 Paenibaci
c	472	16	1.1	3092	8	ZMA17898 Y17898 Zea mays mR
	473	16	1.1	3099	1	BACBGLH D17519 Bacillus ci
	474	16	1.1	3100	2	S67033 S67033 beta-1,3-gl
c	475	16	1.1	3111	1	PSECUME1 D63377 Pseudomonas
	476	16	1.1	3204	40	AF127035 AF127035 Homo sapi
	477	16	1.1	3219	7	SCCDC39 X04289 Yeast cell
c	478	16	1.1	3234	1	PSEPA1G D28587 Pseudomonas
	479	16	1.1	3240	1	SAAJ5198 AJ005198 Streptomy
c	480	16	1.1	3240	1	SAAJ5198 AJ005198 Streptomy
	481	16	1.1	3240	1	SAN6517 AJ006517 Streptomy
c	482	16	1.1	3240	1	SAN6517 AJ006517 Streptomy
	483	16	1.1	3288	10	HSU41387 U41387 Human Gu pr
c	484	16	1.1	3617	12	RATLLIPA L03294 Rattus norv
c	485	16	1.1	3648	34	AB008449 AB008449 Bombyx mo
c	486	16	1.1	3680	8	AF093639 AF093639 Linum usi
c	487	16	1.1	3693	9	HUMPPROA M63635 Human glyci
	488	16	1.1	3720	1	AERPONG X66793 A.eutrophus
	489	16	1.1	3750	35	AF033823 AF033823 Drosophil
c	490	16	1.1	3755	35	AC008239 AC008239 Leishmani
c	491	16	1.1	3762	9	HUMPP M64590 Human glyci
	492	16	1.1	3776	1	CFIB14C L38827 Cellulomona
c	493	16	1.1	3783	9	HUMGDCMR D90239 Human mRNA
	494	16	1.1	3822	7	BLYACL1 M58753 Hordeum vul

	495	16	1.1	3891	35	AF071502
	496	16	1.1	3927	34	AF043629
c	497	16	1.1	4124	7	BOISR
	498	16	1.1	4211	9	HSDRES9
c	499	16	1.1	4307	9	HSTYL
	500	16	1.1	4329	7	AMTAM4
c	501	16	1.1	4348	7	BORR2518
	502	16	1.1	4354	35	MSU09650
c	503	16	1.1	4417	1	AB019513
c	504	16	1.1	4474	5	I58526
c	505	16	1.1	4474	5	I87001
c	506	16	1.1	4509	40	AF168791
c	507	16	1.1	4515	35	AF126540
c	508	16	1.1	4535	40	AF076622
c	509	16	1.1	4607	8	AF093648
c	510	16	1.1	4622	8	AF093641
c	511	16	1.1	4627	8	AF093638
c	512	16	1.1	4631	11	HSU72391
c	513	16	1.1	4637	8	AF093640
c	514	16	1.1	4637	8	AF093643
c	515	16	1.1	4637	8	AF093644
c	516	16	1.1	4651	8	AF093645
c	517	16	1.1	4780	7	ATHTOP2
	518	16	1.1	4809	11	AF038385
c	519	16	1.1	4841	7	LUU27081
	520	16	1.1	4931	1	ECGYRBF
c	521	16	1.1	4970	40	AF107403
	522	16	1.1	4991	1	BLO242596
	523	16	1.1	5029	1	PSETBMAF
c	524	16	1.1	5197	8	LES6379
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	526	16	1.1	5240	12	MMU131021
	527	16	1.1	5263	1	RLRES
c	528	16	1.1	5297	10	HSU61262
c	529	16	1.1	5305	7	CHSOPSA
	530	16	1.1	5390	43	AC009515
c	531	16	1.1	5401	34	DMSLIT
c	532	16	1.1	5479	8	AF093642
c	533	16	1.1	5482	2	BCU19883
	534	16	1.1	5521	2	AF105219
c	535	16	1.1	5541	5	AR012071
c	536	16	1.1	5541	5	AR025196
c	537	16	1.1	5541	5	AR038653
c	538	16	1.1	5541	5	AR068500
	539	16	1.1	5594	1	PPY09450
	540	16	1.1	5708	6	POP29B
	541	16	1.1	5715	9	AB023157
	542	16	1.1	5751	9	HUMMLL
c	543	16	1.1	5924	8	AF093646
	544	16	1.1	6111	10	AB033029
c	545	16	1.1	6125	1	PSEPSTD
c	546	16	1.1	6166	8	AF093649
	547	16	1.1	6296	9	D87432
c	548	16	1.1	6310	4	ACSWSOPS3
	549	16	1.1	6393	1	HIU19730
	550	16	1.1	6536	12	MUSALCR01
	551	16	1.1	6693	35	AF070064
c	552	16	1.1	6751	34	CELMYOD
	553	16	1.1	6940	11	HUMMLLAF4F
c	554	16	1.1	7222	12	MUSMA
c	555	16	1.1	7290	1	BACCCOS
	556	16	1.1	8404	9	HUMHT3I
	557	16	1.1	8421	34	DVU39746
c	558	16	1.1	8766	7	BLYRCABG
	559	16	1.1	8833	11	HUMIP3R3
c	560	16	1.1	9239	1	D85415
	561	16	1.1	9432	5	AR053191
	562	16	1.1	9432	5	I50752
	563	16	1.1	9532	1	MTY20G10
c	564	16	1.1	9677	12	AB009689
c	565	16	1.1	10134	2	AE001488
	566	16	1.1	10326	16	PRSVGEN
	567	16	1.1	10340	2	AE001236

AF071502 Drosophil
AF043629 Toxoplasm
X56978 B.oleracea
X98654 H.sapiens m
X99688 H.sapiens m
X59057 A.majus tra
X60324 B.oleracea
U09650 Manduca sex
AB019513 Streptomy
I58526 Sequence 9
I87001 Sequence 9
AF168791 Homo sapi
AF126540 Drosophil
AF076622 Homo sapi
AF093648 Linum usi
AF093641 Linum usi
AF093638 Linum usi
U72391 Human neoge
AF093640 Linum usi
AF093643 Linum usi
AF093644 Linum usi
AF093645 Linum usi
L21015 Arabidopsis
AF038385 Homo sapi
U27081 Linum usita
X04341 E. coli gen
AF107403 Homo sapi
AJ242596 Bifidobac
L40033 Pseudomonas
AJ006379 Lycopersi
U28219 Treponema p
AJ131021 Mus muscu
X98117 Rhizobium l
U61262 Human neoge
X04131 Spinach pla
AC009515 Staphyloc
X53959 Drosophila
AF093642 Linum usi
U19883 Burkholderi
AF105219 Thermomon
AR012071 Sequence
AR025196 Sequence
AR038653 Sequence
AR068500 Sequence
Y09450 P.putida pl
V01155 Left end of
AB023157 Homo sapi
D14540 Human mRNA
AF093646 Linum usi
AB033029 Homo sapi
D45195 Pseudomonas
AF093649 Linum usi
D87432 Human mRNA
AF134194 Anolis ca
U19730 Haemophilus
L36825 Mus Musculu
AF070064 Drosophil
M59940 Caenorhabdi
L22179 Human MLL-A
D29801 Mouse mRNA
D70843 Bacillus st
D26351 Human mRNA
U39746 Drosophila
M55449 Hordeum vul
U01062 Human type
D85415 Pseudomonas
AR053191 Sequence
I50752 Sequence 1
Z97831 Mycobacteri
AB009689 Mus muscu
AE001488 Helicobac
X97251 Papaya ring
AE001236 Treponema

	568	16	1.1	10437	2	AE000245
c	569	16	1.1	10492	35	DMU34925
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	573	16	1.1	11053	2	AE000286
c	574	16	1.1	11166	2	AE002023
	575	16	1.1	11317	2	AE000945
c	576	16	1.1	11355	2	AE000447
	577	16	1.1	11566	2	U32732
	578	16	1.1	11680	2	AE001258
	579	16	1.1	11694	2	AE000383
	580	16	1.1	11910	9	HUMHRX
c	581	16	1.1	11929	2	AE000496
c	582	16	1.1	11931	12	CGRHOD
	583	16	1.1	12276	43	AC013930
c	584	16	1.1	12323	2	BSP250862
	585	16	1.1	12551	2	AE000598
	586	16	1.1	12663	2	AE000168
	587	16	1.1	12965	2	AE002048
c	588	16	1.1	13163	2	AE001042
c	589	16	1.1	13638	11	AC005573
c	590	16	1.1	13831	2	AE000707
c	591	16	1.1	14097	2	AE001093
	592	16	1.1	14255	5	I43726
	593	16	1.1	14255	5	I43760
	594	16	1.1	14255	5	I96218
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c	596	16	1.1	14529	34	CET25G3
	597	16	1.1	14930	1	D90834
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	599	16	1.1	15605	1	D90833
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	601	16	1.1	15705	1	D90788
c	602	16	1.1	15807	1	MEU72662
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	604	16	1.1	16637	41	AC010371
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	606	16	1.1	17871	1	D90703
	607	16	1.1	18227	12	AF110420
	608	16	1.1	18292	2	SCF76
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	614	16	1.1	20042	44	AC016569
	615	16	1.1	20278	2	AE001209
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	618	16	1.1	21038	41	AC008593
	619	16	1.1	21189	34	CEF14B4
	620	16	1.1	21589	41	AC010381
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c	622	16	1.1	21839	1	PPSURFOP
	623	16	1.1	22145	8	ATF3I3
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	625	16	1.1	22916	34	CEF53H10
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	627	16	1.1	23476	7	AB025641
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c	629	16	1.1	23906	2	AF176314
c	630	16	1.1	24411	41	AC008534
	631	16	1.1	24555	45	AC017315
c	632	16	1.1	25252	2	AF140550
	633	16	1.1	25339	34	AB017765
c	634	16	1.1	25795	41	AC008911
	635	16	1.1	26007	1	BSY14083
	636	16	1.1	26402	43	AC013906
c	637	16	1.1	26463	43	AC012932
	638	16	1.1	26536	2	AE001244
c	639	16	1.1	27060	43	AC014005
c	640	16	1.1	27555	43	AC012903

AE000245 Escherich
U34925 Drosophila
Y14077 Bacillus su
AE000163 Escherich
AE000418 Escherich
AE000286 Escherich
AE002023 Deinococc
AE000945 Archaeogl
AE000447 Escherich
U32732 Haemophilus
AE001258 Treponema
AE000383 Escherich
L04284 Human germl
AE000496 Escherich
X61084 C.griseus r
AC013930 Drosophil
AJ250862 Bacillus
AE000598 Helicobac
AE000168 Escherich
AE002048 Deinococc
AE001042 Archaeogl
AC005573 Homo sapi
AE000707 Aquifex a
AE001093 Archaeogl
I43726 Sequence 1
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I96218 Sequence 55
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Z72516 Caenorhabdi
D90834 E.coli geno
AC013987 Drosophil
D90833 E.coli geno
AE000968 Archaeogl
D90788 E.coli geno
U72662 Methylobact
AC010290 Homo sapi
AC010371 Homo sapi
AC012987 Drosophil
D90703 Escherichia
AF110420 Mus muscu
AL121600 Streptomy
D90704 Escherichia
D90789 E.coli geno
D90700 Escherichia
AE001708 Thermotog
AC010229 Homo sapi
AC016569 Homo sapi
AE001209 Treponema
U56960 Caenorhabdi
Z68341 Caenorhabdi
AC008593 Homo sapi
Z75535 Caenorhabdi
AC010381 Homo sapi
L32093 Pediococcus
Z32771 P.pentosace
AL080237 Arabidops
D83967 Bacillus su
Z77664 Caenorhabdi
AC014464 Drosophil
AB025641 Arabidops
Z69368 S.pombe chr
AF176314 Zymomonas
AC008534 Homo sapi
AC017315 Drosophil
AF140550 Salmonell
AB017765 Trypanoso
AC008911 Homo sapi
Y14083 Bacillus su
AC013906 Drosophil
AC012932 Drosophil
AE001244 Treponema
AC014005 Drosophil
AC012903 Drosophil

	641	16	1.1	27602	34	CET01C1 Z68010 Caenorhabdi
	642	16	1.1	28168	34	CEY37H9A AL032625 Caenorhab
c	643	16	1.1	29624	35	CELB0545 AF078781 Caenorhab
c	644	16	1.1	30034	8	OSU70541 U70541 Oryza sativ
	645	16	1.1	30148	34	CEF57C7 Z69646 Caenorhabdi
	646	16	1.1	30419	35	CELT07H8 AF067945 Caenorhab
c	647	16	1.1	30941	1	SC4C6 AL079355 Streptomy
	648	16	1.1	31312	10	AP000283 AP000283 Homo sapi
	649	16	1.1	31638	1	RMEXPGNS Z79692 R.meliloti
c	650	16	1.1	31795	34	CELT07H6 U53344 Caenorhabdi
	651	16	1.1	31913	43	AC013216 AC013216 Drosophil
c	652	16	1.1	31975	8	SPCC553 AL023704 S.pombe c
c	653	16	1.1	32039	1	SC7A1 AL034447 Streptomy
	654	16	1.1	32106	10	AP000284 AP000284 Homo sapi
	655	16	1.1	32195	20	AC004154 Ac004154 Drosophil
c	656	16	1.1	32566	34	CEY94A7B AL023856 Caenorhab
c	657	16	1.1	32806	32	HSJ819L10 AL132767 Homo sapi
c	658	16	1.1	33550	11	AC003004 AC003004 Human Chr
c	659	16	1.1	33896	35	CELT05A8 AF040652 Caenorhab
c	660	16	1.1	33930	34	CEK04H4 Z27078 Caenorhabdi
c	661	16	1.1	33954	7	SC9905 Z46861 S.cerevisia
	662	16	1.1	34083	2	AF124757 AF124757 Zymomonas
c	663	16	1.1	34150	1	MTCY190 Z70283 Mycobacteri
	664	16	1.1	34238	32	CEY45F10_4 Continuation (5 of
c	665	16	1.1	34774	43	AC013899 AC013899 Drosophil
c	666	16	1.1	34860	34	CELR173 U39743 Caenorhabdi
	667	16	1.1	35292	1	MTCY3C7 Z82098 Mycobacteri
	668	16	1.1	35424	43	AC013816 AC013816 Homo sapi
	669	16	1.1	35559	6	PABY13918 Y13918 Pseudomonas
	670	16	1.1	35580	6	AB008550 AB008550 Pseudomon
	671	16	1.1	35737	11	AC005263 AC005263 Homo sapi
	672	16	1.1	35743	34	CELF31E8 U55856 Caenorhabdi
	673	16	1.1	35769	8	SPAC23A1 AL021813 S.pombe c
	674	16	1.1	36330	1	MTY20B11 Z95121 Mycobacteri
c	675	16	1.1	36615	43	AC014144 AC014144 Drosophil
c	676	16	1.1	37186	1	MSGY244 AD000003 Mycobacte
c	677	16	1.1	37218	11	HSN11D4 Z68285 Human DNA s
c	678	16	1.1	37225	34	CEC17E4 Z81037 Caenorhabdi
	679	16	1.1	37307	10	HS335H7 AL031258 Human DNA
c	680	16	1.1	37394	8	SPAC2F3 Z99165 S.pombe chr
	681	16	1.1	37439	34	CEF35E2 Z81528 Caenorhabdi
	682	16	1.1	37462	43	AC013090 AC013090 Drosophil
	683	16	1.1	37470	35	CELH14E04 AF125448 Caenorhab
c	684	16	1.1	37693	10	AP000522 AP000522 Homo sapi
c	685	16	1.1	37821	1	MLCB1770 Z70722 Mycobacteri
c	686	16	1.1	38548	8	SPBC21B10 AL121794 S.pombe c
c	687	16	1.1	38563	34	CET20B3 Z81593 Caenorhabdi
	688	16	1.1	38715	11	AC000092 AC000092 Homo sapi
c	689	16	1.1	39146	10	CH19R28051 AD000864 Homo sapi
c	690	16	1.1	39480	34	CEC34C6 Z66494 Caenorhabdi
	691	16	1.1	39752	35	CELC04F5 AF101305 Caenorhab
	692	16	1.1	39839	43	AC013000 AC013000 Drosophil
	693	16	1.1	40018	7	AP000740 AP000740 Arabidops
	694	16	1.1	40162	40	U58675 U58675 Homo sapien
	695	16	1.1	40320	43	AC015387 AC015387 Drosophil
	696	16	1.1	40397	7	SC9959 Z49939 S.cerevisia
	697	16	1.1	40442	2	SCI8 AL132644 Streptomy
	698	16	1.1	40665	35	CELC27F2 U40419 Caenorhabdi
c	699	16	1.1	40665	35	CELC27F2 U40419 Caenorhabdi
	700	16	1.1	40880	7	SPCC1235 AL031764 S.pombe c
c	701	16	1.1	40965	42	AC012633 AC012633 Homo sapi
	702	16	1.1	41009	32	CEY94A7 Z99294 Caenorhabdi
c	703	16	1.1	41037	45	AC017476 AC017476 Drosophil
	704	16	1.1	41071	34	CELB0303 M77697 C.elegans c
c	705	16	1.1	41397	34	CEB0285 Z34533 Caenorhabdi
	706	16	1.1	41594	41	AC010964 AC010964 Homo sapi
c	707	16	1.1	41625	1	SCH24 AL049826 Streptomy
c	708	16	1.1	41625	10	HSS171R AJ239328 Homo sapi
c	709	16	1.1	41848	33	AC006098 AC006098 Homo sapi
	710	16	1.1	41906	1	SC5C7 AL031515 Streptomy
c	711	16	1.1	42282	34	CELB0304 U39472 Caenorhabdi
c	712	16	1.1	42418	32	HSN38G6 Z96802 Homo sapien
c	713	16	1.1	42660	34	CEF15D3 Z81063 Caenorhabdi
	714	16	1.1	42729	1	MTCY71 Z92771 Mycobacteri
c	715	16	1.1	42776	34	CEF15D4 Z80344 Caenorhabdi
	716	16	1.1	42968	34	CEY37A1A Z99270 Caenorhabdi
	717	16	1.1	43075	6	U88974 U88974 Streptococc
c	718	16	1.1	43190	11	AC005777 AC005777 Homo sapi
	719	16	1.1	43430	1	MTCY16B7 Z81331 Mycobacteri
c	720	16	1.1	43516	10	AP000401 AP000401 Homo sapi
	721	16	1.1	44090	33	AC006784 AC006784 Caenorhab
	722	16	1.1	44725	40	AF036405 AF036405 Homo sapi
	723	16	1.1	45000	43	AC013257 AC013257 Leishmani
c	724	16	1.1	45701	43	AC014674 AC014674 Drosophil
c	725	16	1.1	45932	43	AC015155 AC015155 Drosophil
c	726	16	1.1	46375	6	AF064539 AF064539 Bacteriop
c	727	16	1.1	46445	2	AF051917 AF051917 Staphyloc
c	728	16	1.1	46582	43	AC012831 AC012831 Drosophil
	729	16	1.1	47263	41	AC010425 AC010425 Homo sapi
	730	16	1.1	47815	41	AC009563 AC009563 Homo sapi
	731	16	1.1	47852	1	MTV023 AL022022 Mycobacte
c	732	16	1.1	48295	44	AC010749 AC010749 Homo sapi
	733	16	1.1	48574	44	AC016602 AC016602 Homo sapi
c	734	16	1.1	49027	42	AC011727 AC011727 Homo sapi
	735	16	1.1	50149	44	AC016083 AC016083 Homo sapi
	736	16	1.1	50302	45	AC017148 AC017148 Drosophil
c	737	16	1.1	50969	43	AC014793 AC014793 Drosophil
	738	16	1.1	50997	41	AC010679_3 Continuation (4 of
c	739	16	1.1	52001	11	HSBG91O18 AL080238 Human DNA
	740	16	1.1	52094	32	T16I18 AL049915 Arabidops
	741	16	1.1	52297	6	MLCGA Z18946 Mycobacteri
	742	16	1.1	54252	7	AB017060 AB017060 Arabidops
	743	16	1.1	54488	43	AC013814 AC013814 Homo sapi
c	744	16	1.1	54527	43	AC015174 AC015174 Drosophil
	745	16	1.1	55466	43	AC013616 AC013616 Homo sapi
	746	16	1.1	57166	40	AC009320 AC009320 Homo sapi
c	747	16	1.1	57236	42	AC009878 AC009878 Homo sapi
	748	16	1.1	57352	44	AC016317 AC016317 Homo sapi
c	749	16	1.1	57517	42	AC010563 AC010563 Drosophil
	750	16	1.1	57634	42	AC010702 AC010702 Drosophil
	751	16	1.1	58527	7	AB007649 AB007649 Arabidops
	752	16	1.1	58713	41	AC009494 AC009494 Homo sapi
c	753	16	1.1	58903	44	AC016104 AC016104 Homo sapi
c	754	16	1.1	61151	44	AC016416 AC016416 Homo sapi
c	755	16	1.1	61845	43	AC013765 AC013765 Homo sapi
c	756	16	1.1	62198	43	AC013832 AC013832 Drosophil
c	757	16	1.1	62608	44	AC016784 AC016784 Homo sapi
c	758	16	1.1	62944	10	HSMHC3W5A U89336 Human HLA c
c	759	16	1.1	62953	43	AC016121 AC016121 Homo sapi
	760	16	1.1	63441	45	AC012554 AC012554 Homo sapi
	761	16	1.1	63681	43	AC015996 AC015996 Homo sapi
	762	16	1.1	63751	45	AC017489 AC017489 Drosophil
c	763	16	1.1	64044	8	SCE9163 U18922 Saccharomyc
c	764	16	1.1	64211	40	AC000054 AC000054 , complet
c	765	16	1.1	64797	8	SCE9747 U18839 Saccharomyc
	766	16	1.1	64957	1	AB032367 AB032367 Streptomy
	767	16	1.1	67042	41	AC009939 AC009939 Homo sapi
c	768	16	1.1	67042	41	AC009939 AC009939 Homo sapi
c	769	16	1.1	68203	42	AC012427 AC012427 Homo sapi
c	770	16	1.1	68726	7	AB017063 AB017063 Arabidops
c	771	16	1.1	69493	43	AC014818 AC014818 Drosophil
c	772	16	1.1	69516	45	AC016851 AC016851 Homo sapi
c	773	16	1.1	69673	2	AF102990 AF102990 Yersinia
	774	16	1.1	70095	41	AC008980 AC008980 Homo sapi
c	775	16	1.1	70311	8	AF128457 AF128457 Oryza sat
c	776	16	1.1	70661	44	AC016422 AC016422 Homo sapi
c	777	16	1.1	70865	43	AC015476 AC015476 Homo sapi
	778	16	1.1	71097	8	F15K9 AC005278 Arabidops
c	779	16	1.1	71214	45	AC017250 AC017250 Drosophil
	780	16	1.1	71907	43	AC014585 AC014585 Drosophil
c	781	16	1.1	72164	32	HS409J21 Z83824 Homo sapien
c	782	16	1.1	72401	41	AC008389 AC008389 Homo sapi
c	783	16	1.1	72438	2	ECOUW67_3 Continuation (4 of
c	784	16	1.1	72924	43	AC015889 AC015889 Homo sapi
	785	16	1.1	72975	44	AC016354 AC016354 Homo sapi
c	786	16	1.1	73087	10	HS147M19 AL021978 Homo sapi

c 787	16	1.1	73491	43	AC009641	AC009641 Homo sapi
c 788	16	1.1	73635	50	ATAC011915	AC011915 Arabidops
789	16	1.1	73739	35	AC001646	AC001646 Drosophil
c 790	16	1.1	74780	33	AC005445	AC005445 Drosophil
c 791	16	1.1	75079	43	AC015047	AC015047 Drosophil
792	16	1.1	75263	41	AC009835	AC009835 Homo sapi
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794	16	1.1	76743	35	AC005473	AC005473 Drosophil
795	16	1.1	77618	45	AC017020	AC017020 Homo sapi
c 796	16	1.1	78189	44	AC015737	AC015737 Homo sapi
c 797	16	1.1	78205	43	AC015748	AC015748 Homo sapi
c 798	16	1.1	78505	33	AC006408	AC006408 Homo sapi
799	16	1.1	79109	7	AB016871	AB016871 Arabidops
c 800	16	1.1	79114	33	AC005475	AC005475 Drosophil
801	16	1.1	79227	10	HS148E22	AL008725 Human DNA
c 802	16	1.1	79528	11	HS466N1	Z97630 Human DNA s
c 803	16	1.1	79706	7	AB020746	AB020746 Arabidops
c 804	16	1.1	79740	42	AC009905	AC009905 Drosophil
805	16	1.1	80000	46	AC005652	Ac005652 *** SEQUE
c 806	16	1.1	80389	35	AC005643	AC005643 Drosophil
c 807	16	1.1	80393	7	AP000382	AP000382 Arabidops
808	16	1.1	80446	35	AC004288	AC004288 Drosophil
c 809	16	1.1	80818	42	AC009732	AC009732 Drosophil
c 810	16	1.1	81487	11	HSJ770C23	AL118509 Human DNA
c 811	16	1.1	81786	11	AC003002	AC003002 Human DNA
c 812	16	1.1	82359	40	AC004922	AC004922 Homo sapi
c 813	16	1.1	82503	7	AB016886	AB016886 Arabidops
c 814	16	1.1	83253	7	AP000383	AP000383 Arabidops
c 815	16	1.1	83605	43	AC014199	AC014199 Drosophil
816	16	1.1	83693	8	ATT13J8	AL035524 Arabidops
c 817	16	1.1	83922	8	T9A4	AF096373 Arabidops
818	16	1.1	84246	34	AC002512	AC002512 Drosophil
c 819	16	1.1	84305	41	AC006943	AC006943 Mus muscu
c 820	16	1.1	84323	10	HS138B7	Z98752 Human DNA s
c 821	16	1.1	85561	8	ATAC009326	AC009326 Arabidops
c 822	16	1.1	85674	40	AF164343	AF164343 Homo sapi
c 823	16	1.1	85740	43	AC014942	AC014942 Drosophil
c 824	16	1.1	86643	42	AC012321	AC012321 Homo sapi
825	16	1.1	86699	7	AB009050	AB009050 Arabidops
c 826	16	1.1	87077	40	HUAC004097	AC004097 Human Chr
827	16	1.1	87210	7	AB011485	AB011485 Arabidops
828	16	1.1	88178	44	AC011787	AC011787 Homo sapi
829	16	1.1	88413	8	ATAC005724	AC005724 Arabidops
c 830	16	1.1	88512	8	F21H2	AC007894 Arabidops
831	16	1.1	89086	10	HS1188J21	AL109963 Human DNA
c 832	16	1.1	89448	40	AC005067	AC005067 Homo sapi
c 833	16	1.1	90390	42	AC009377	AC009377 Drosophil
834	16	1.1	91813	42	AC010716	AC010716 Drosophil
c 835	16	1.1	91863	8	ATAC004667	AC004667 Arabidops
c 836	16	1.1	92472	10	HS181C9	Z98743 Human DNA s
837	16	1.1	92948	8	ATAF000657	AF000657 Arabidops
c 838	16	1.1	93131	43	AC000105	AC000105 Homo sapi
c 839	16	1.1	93655	42	AC010559	AC010559 Drosophil
c 840	16	1.1	93845	8	ATAC004684	AC004684 Arabidops
841	16	1.1	94386	11	HS452M16	AL024493 Human DNA
842	16	1.1	96460	11	HS633O20	AL023804 Human DNA
843	16	1.1	96679	8	ATT8P19	AL133315 Arabidops
844	16	1.1	96801	8	ATAC003033	AC003033 Arabidops
c 845	16	1.1	96924	45	AC017831	AC017831 Drosophil
c 846	16	1.1	96953	41	AC011428	AC011428 Homo sapi
c 847	16	1.1	97146	8	AC007259	AC007259 Arabidops
848	16	1.1	97308	43	AC013925	AC013925 Drosophil
849	16	1.1	97693	40	AC002383	AC002383 Homo sapi
c 850	16	1.1	98052	10	AP000219	AP000219 Homo sapi
c 851	16	1.1	98052	10	AP000341	AP000341 Homo sapi
c 852	16	1.1	98124	8	ATT16L1	AL031394 Arabidops
c 853	16	1.1	98695	35	AC005556	AC005556 Drosophil
854	16	1.1	99384	8	AF076243	AF076243 Arabidops
c 855	16	1.1	99416	8	AC009398	AC009398 Genomic s
856	16	1.1	99856	8	ATF24G24	AL049488 Arabidops
c 857	16	1.1	100000	9	AB020860	AB020860 Homo sapi
858	16	1.1	100000	10	AP000040	AP000040 Homo sapi
c 859	16	1.1	100000	10	AP000069	AP000069 Homo sapi
860	16	1.1	100000	10	AP000109	AP000109 Homo sapi
861	16	1.1	100000	10	AP000131	AP000131 Homo sapi
862	16	1.1	100000	10	AP000153	AP000153 Homo sapi
863	16	1.1	100000	10	AP000185	AP000185 Homo sapi
864	16	1.1	100000	10	AP000209	AP000209 Homo sapi
865	16	1.1	100201	41	AC008366	AC008366 Drosophil
c 866	16	1.1	100364	40	AC007590	AC007590 Homo sapi
867	16	1.1	100509	42	AC010023	AC010023 Drosophil
c 868	16	1.1	101340	45	AC018104	AC018104 Drosophil
c 869	16	1.1	102004	8	ATAC005395	AC005395 Arabidops
870	16	1.1	102739	11	HS671O14	AL031595 Human DNA
c 871	16	1.1	103370	41	AC009352	AC009352 Drosophil
872	16	1.1	103632	8	AF074021	AF074021 Arabidops
c 873	16	1.1	104059	42	AC010110	AC010110 Drosophil
c 874	16	1.1	104081	11	HSDJ263J7	AL049545 Human DNA
875	16	1.1	104163	50	AC010155	AC010155 Genomic s
c 876	16	1.1	105126	43	AC014828	AC014828 Drosophil
c 877	16	1.1	105320	32	AP000668	AP000668 Homo sapi
c 878	16	1.1	105788	32	AP000749	AP000749 Homo sapi
c 879	16	1.1	105809	43	AC013758	AC013758 Homo sapi
880	16	1.1	105816	45	AC017069	AC017069 Homo sapi
881	16	1.1	106273	11	HSJ1018A4	AL109612 Human DNA
882	16	1.1	106723	42	AC010064	AC010064 Drosophil
883	16	1.1	106953	33	AC006982	AC006982 Homo sapi
884	16	1.1	108879	11	AC004804	AC004804 Homo sapi
885	16	1.1	108906	32	AP000796	AP000796 Homo sapi
c 886	16	1.1	109566	33	AC007803	AC007803 Drosophil
c 887	16	1.1	109826	33	AC008311	AC008311 Drosophil
c 888	16	1.1	110000	32	CEY102A5_0	Z99711 Caenorhabdi
889	16	1.1	110000	32	CEY116A8_2	Continuation (3 of
890	16	1.1	110000	32	CEY37H9_0	AL022596 Caenorhab
c 891	16	1.1	110000	32	CEY47H9_1	Continuation (2 of
892	16	1.1	110000	32	CEY47H9_3	Continuation (4 of
893	16	1.1	110000	32	CEY48G10_1	Continuation (2 of
894	16	1.1	110000	32	CEY53C10_0	Z93340 Caenorhabdi
895	16	1.1	110000	32	CEY53C10_1	Continuation (2 of
896	16	1.1	110000	32	CEY53C10_3	Continuation (4 of
c 897	16	1.1	110000	32	CEY73F8_1	Continuation (2 of
c 898	16	1.1	110000	32	CEY81G3_2	Continuation (3 of
899	16	1.1	110000	33	AC007194_1	Continuation (2 of
c 900	16	1.1	110000	41	AC008691_1	Continuation (2 of
c 901	16	1.1	110000	41	AC011455_0	AC011455 Homo sapi
902	16	1.1	110926	41	AC009846	AC009846 Drosophil
c 903	16	1.1	111723	11	HSJ101K10	AL080276 Human DNA
904	16	1.1	111732	33	AC006015	AC006015 Homo sapi
905	16	1.1	112074	9	AP000012	AP000012 Homo sapi
906	16	1.1	112710	32	HSJ136O14	AL121963 Homo sapi
c 907	16	1.1	112710	42	AC011252	AC011252 Drosophil
c 908	16	1.1	112753	41	AC009459	AC009459 Drosophil
909	16	1.1	112789	33	AL133341	AL133341 Homo sapi
c 910	16	1.1	113220	42	AC009368	AC009368 Drosophil
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c 912	16	1.1	113687	40	AC005301	AC005301 Homo sapi
913	16	1.1	114567	41	AC009417	AC009417 Homo sapi
914	16	1.1	115118	10	AP000247	AP000247 Homo sapi
c 915	16	1.1	115319	43	AF202962	AF202962 Homo sapi
c 916	16	1.1	115907	33	HSJ651E10	AL122002 Homo sapi
c 917	16	1.1	115962	41	AC008441	AC008441 Homo sapi
c 918	16	1.1	116828	32	HSJ272H18	AL109826 Homo sapi
c 919	16	1.1	116868	42	AC010029	AC010029 Drosophil
920	16	1.1	117696	42	AC010750	AC010750 Drosophil
c 921	16	1.1	118067	10	HS163M9	AL021920 Homo sapi
c 922	16	1.1	118100	45	AC017911	AC017911 Drosophil
923	16	1.1	118235	12	AC003060	AC003060 Mus muscu
c 924	16	1.1	118831	11	HS989H11	Z83851 Human DNA s
c 925	16	1.1	119001	8	ATAC005896	AC005896 Arabidops
c 926	16	1.1	119122	42	AC010003	AC010003 Drosophil
927	16	1.1	119348	42	AC009369	AC009369 Drosophil
c 928	16	1.1	119399	33	AC007757	AC007757 Drosophil
c 929	16	1.1	119430	8	ATF9D16	AL035394 Arabidops
c 930	16	1.1	119751	33	AC007755	AC007755 Drosophil
c 931	16	1.1	122228	10	AC000003	AC000003 Homo sapi
932	16	1.1	123091	34	CEY87G2A	AL110500 Caenorhab

c 933	16	1.1	123360	10	HS222E13	Z93241 Human DNA s
c 934	16	1.1	123421	33	AC007756	AC007756 Drosophil
c 935	16	1.1	123551	33	AC005809	AC005809 Homo sapi
936	16	1.1	123737	41	AF189001	AF189001 Homo sapi
c 937	16	1.1	123947	40	AC005045	AC005045 Homo sapi
c 938	16	1.1	124539	33	AC008043	AC008043 Drosophil
c 939	16	1.1	125010	41	AC011394	AC011394 Homo sapi
c 940	16	1.1	125235	33	AC008197	AC008197 Drosophil
941	16	1.1	125368	42	AC008929	AC008929 Homo sapi
942	16	1.1	125729	11	HS971N18	AL021396 Human DNA
943	16	1.1	126356	33	AC006876	AC006876 Caenorhab
c 944	16	1.1	127168	10	HS1163J1	AL031588 Human DNA
c 945	16	1.1	127282	11	AC005155	AC005155 Homo sapi
946	16	1.1	127528	33	AC007821	AC007821 Drosophil
947	16	1.1	128150	8	AC007661	AC007661 Arabidops
948	16	1.1	128447	33	AC006490	AC006490 Drosophil
949	16	1.1	128598	1	D90912	D90912 Synechocyst
950	16	1.1	128765	40	HUAC002040	AC002040 Homo sapi
951	16	1.1	128992	33	HS223B1	AL031943 Homo sapi
952	16	1.1	129138	33	AC008205	AC008205 Drosophil
953	16	1.1	129191	42	AC009751	AC009751 Drosophil
954	16	1.1	129238	41	AC011469	AC011469 Homo sapi
955	16	1.1	129779	35	AC006214	AC006214 Drosophil
c 956	16	1.1	130142	45	AC017890	AC017890 Drosophil
957	16	1.1	130536	44	AC007807	AC007807 Drosophil
958	16	1.1	130583	41	AC007420	AC007420 Drosophil
959	16	1.1	130608	16	AF005370	AF005370 Alcelaphi
c 960	16	1.1	131024	33	AC004666	AC004666 Homo sapi
c 961	16	1.1	131410	44	AC008319	AC008319 Drosophil
962	16	1.1	131973	44	AF205589	AF205589 Homo sapi
c 963	16	1.1	132025	33	AC007824	AC007824 Drosophil
964	16	1.1	132418	33	AC006357	AC006357 Homo sapi
c 965	16	1.1	133772	43	AC010211	AC010211 Drosophil
966	16	1.1	134963	10	HS199L16	AL022151 Human DNA
967	16	1.1	135258	10	HS127B20	Z83838 Human DNA s
c 968	16	1.1	135296	42	AC010567	AC010567 Drosophil
c 969	16	1.1	135567	33	AC008235	AC008235 Drosophil
970	16	1.1	135648	11	AC004069	AC004069 Homo sapi
971	16	1.1	136145	41	AC008962	AC008962 Homo sapi
c 972	16	1.1	136200	33	AC008204	AC008204 Drosophil
c 973	16	1.1	136254	1	ECOUW82	L10328 E. coli; th
974	16	1.1	136742	1	ECU82598	U82598 Escherichia
c 975	16	1.1	136742	1	ECU82598	U82598 Escherichia
976	16	1.1	136955	33	HSDJ306F2	AL121573 Homo sapi
977	16	1.1	137177	33	AC008189	AC008189 Drosophil
978	16	1.1	137654	32	AP000713	AP000713 Homo sapi
979	16	1.1	137974	42	AC010046	AC010046 Drosophil
c 980	16	1.1	138285	42	AC010047	AC010047 Drosophil
c 981	16	1.1	139415	42	AC012291	AC012291 Homo sapi
c 982	16	1.1	139480	43	AC012837	AC012837 Drosophil
983	16	1.1	139801	10	CNS01DS3	AL121653 BAC seque
c 984	16	1.1	139825	43	AC010919	AC010919 Drosophil
c 985	16	1.1	140331	40	AC007002	AC007002 Homo sapi
c 986	16	1.1	140942	10	AC002525	AC002525 Human PAC
987	16	1.1	141320	45	AC017833	AC017833 Drosophil
988	16	1.1	141744	1	ECU28377	U28377 Escherichia
989	16	1.1	142418	7	AP000815	AP000815 Oryza sat
c 990	16	1.1	142660	43	AC010968	AC010968 Homo sapi
c 991	16	1.1	142852	8	AF161269	AF161269 Oryza sat
992	16	1.1	143131	33	AC007039	AC007039 Homo sapi
c 993	16	1.1	143774	32	HSP10238	AL109763 Homo sapi
994	16	1.1	144673	43	AC012239	AC012239 Homo sapi
995	16	1.1	144720	41	AC009177	AC009177 Arabidops
996	16	1.1	145531	42	AC011180	AC011180 Homo sapi
997	16	1.1	146153	35	AC007452	AC007452 Drosophil
c 998	16	1.1	146458	33	AL133290	AL133290 Homo sapi
999	16	1.1	146497	33	AC007718	AC007718 Homo sapi
1000	16	1.1	146858	33	AC006457	AC006457 Homo sapi

ALIGNMENTS

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RESULT   1
AG2H417/c
LOCUS       AG2H417        91 bp    DNA             INV       29-APR-1996
DEFINITION  A.gambiae satellite DNA (locus AG2H417).
ACCESSION   Z72082
VERSION     Z72082.1  GI:1292591
KEYWORDS    satellite.
SOURCE      African malaria mosquito.
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Diptera; Nematocera; Culicoidea; Culicidae; Anopheles.
REFERENCE   1  (bases 1 to 91)
  AUTHORS   Zheng,L., Benedict,M.Q., Cornel,A.J., Collins,F.H. and Kafatos,F.C.
  TITLE     An integrated genetic map of the African human malaria vector
            mosquito, Anopheles gambiae
  JOURNAL   Genetics 143 (1996) In press
REFERENCE   2  (bases 1 to 91)
  AUTHORS   Zheng,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-APR-1996) Zheng L., European Molecular Biology
            Laboratory, Meyerhofstrasse 1, 69117 Heidelberg, FRG
FEATURES             Location/Qualifiers
     source          1. .91
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                     /strain="Suakoko"
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                     /chromosome="2"
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                     /clone_lib="phage M13"
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     satellite       1. .91
                     /note="locus AG2H417"
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ORIGIN


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  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1270 acccttcagacacataccgacag 1292
           |||||||||||||||||||||||
Db     64 ACCCTTCAGACACATACCGACAG 42


RESULT   2
AG2H442/c
LOCUS       AG2H442        93 bp    DNA             INV       29-APR-1996
DEFINITION  A.gambiae satellite DNA (locus AG2H442).
ACCESSION   Z72084
VERSION     Z72084.1  GI:1292593
KEYWORDS    satellite.
SOURCE      African malaria mosquito.
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Diptera; Nematocera; Culicoidea; Culicidae; Anopheles.
REFERENCE   1  (bases 1 to 93)
  AUTHORS   Zheng,L., Benedict,M.Q., Cornel,A.J., Collins,F.H. and Kafatos,F.C.
  TITLE     An integrated genetic map of the African human malaria vector
            mosquito, Anopheles gambiae
  JOURNAL   Genetics 143 (1996) In press
REFERENCE   2  (bases 1 to 93)
  AUTHORS   Zheng,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-APR-1996) Zheng L., European Molecular Biology
            Laboratory, Meyerhofstrasse 1, 69117 Heidelberg, FRG
FEATURES             Location/Qualifiers
     source          1. .93
                     /organism="Anopheles gambiae"
                     /strain="Suakoko"
                     /db_xref="taxon:7165"
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                     /dev_stage="adult"
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                     /clone="pAG442"
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                     /note="polytene 7"
     satellite       1. .93
                     /note="locus AG2H442"
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  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1270 acccttcagacacataccgacag 1292
          |||||||||||||||||||||||
Db     62 ACCCTTCAGACACATACCGACAG 40
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RESULT   3
GGU72352
LOCUS       GGU72352     1435 bp    mRNA            VRT       01-JUL-1997
DEFINITION  Gallus gallus serine protease mRNA, partial cds.
ACCESSION   U72352
VERSION     U72352.1  GI:2228535
KEYWORDS    .
SOURCE      chicken.
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
            Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1435)
  AUTHORS   Kirby,M.L., Wallis,K.T., Rhodes,M.R, Stadt,H.A., Kumiski,D.H.,
            Li,Y.X. and Lei,C.-L.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1996) Institute of Molecular Medicine and
            Genetics, Medical College of Georgia, Laney Walker Blvd, Augusta,
            GA 30912, USA
FEATURES             Location/Qualifiers
     source          1. .1435
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                     /strain="Arbor Acre"
                     /db_xref="taxon:9031"
                     /dev_stage="embryo"
                     /tissue_type="neural crest"
     CDS             <1. .1212
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                     IPSDRLRKFLQKEEERKSSWFGNAETKRRYIGVMMLTLTPQHPAELKLRDPSFPDVSY
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                     LLVSVVPEVTE"
BASE COUNT       260 a    451 c    466 g    258 t
ORIGIN
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  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    817 ggcatctcctttgccatccc 836
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Db    814 GGCATCTCCTTTGCCATCCC 833
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RESULT   4
GOGDH
LOCUS       GOGDH        2890 bp    DNA
DEFINITION  G.oxydans gdh gene.
ACCESSION   X62710 S60040
VERSION     X62710.1  GI:58416
KEYWORDS    coenzyme PQQ; gdh gene; gluconic acid
            dehydrogenase; quinoprotein.
SOURCE      Gluconobacter oxydans.
  ORGANISM  Gluconobacter oxydans
            Bacteria; Proteobacteria; alpha subd:
            Gluconobacter.
REFERENCE   1  (bases 1 to 2890)
  AUTHORS   Cleton-Jansen,A.M., Dekker,S., van de
  TITLE     A single amino acid substitution char
            of quinoprotein glucose dehydrogenase in Gluconobacter oxydans
  JOURNAL   Mol. Gen. Genet. 229 (2), 206-212 (1991)
  MEDLINE   92017653
REFERENCE   2  (bases 1 to 2890)
  AUTHORS   Goosen,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-FEB-1992) N. Goosen, Dept of Mol Genetics, Gorlaeus
            Laboratories, Leiden University, P O Box 9502, 2300 RA Leiden, THE
            NETHERLANDS
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:442"
     RBS             242. .245
     gene            251. .2677
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                     LLPFVSRARSVARGRPSCRSPAVGVAVLALFASLFTDPHDISGELPTQIANASPADPD
                     NVPASEWHAYGRTQAGDRWSPLNQINATNVSNLKVAWHIHTKDMMNSNDPGEATNEAT
                     PIEFNNTLYMCSLHQKLFAVDGATGNVKWVYDPKLQINPGFQHLTCRGVSFHETPANA
                     MDSDGNPAPTDCAKDSILPVNDGRLVEVDADTGKTCSGFGNNGEIDLRVPNQPYTTPG
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                     NADTGKLAWFYQTVHHDLWDMELPSQPSLVDVTQKDGTLVPAIYAPTKTGDIFVLDRR
                     TGKEIVPAPETPVPQGAAPGDHTSPTQPMSQLTLRPKNPLNDSDIWGGTIFDQMFCSI
                     YFHTLRYEGPFTPPSLKGSLIFPGDLGMFEWGGLAVDPQRQVAFANPISLPFVSQLVP
                     RGPGNPLWPEENAKGTGGETGLQHNYGIPYAVNLHPFLDPVLLPFGIKMPCRTPPWGY
                     VAGIDLKTNKVVWQHRNGTLRDSMYGSSLPIPLPPIKIGVPSLGGPLSTAGNLGFLTA
                     SMDYYIRAYNLTTGKVLWQDRLPAGAQATPITYAINGKQYIVTYAGGHNSFPTRMGDD
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                     /note="membrane spanning fragment"
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BASE COUNT       555 a    975 c    786 g    574 t
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  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    597 atgggtcgctgccatcggcg 616
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Db    340 ATGGGTCGCTGCCATCGGCG 359
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RESULT   5
AC013843/c
LOCUS       AC013843    31427 bp    DNA             HTG       16-NOV-1999
DEFINITION  Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
            pieces.
ACCESSION   AC013843
VERSION     AC013843.1  GI:6437492
KEYWORDS    HTG; HTGS_PHASE2.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 31427)
  AUTHORS   Adams,M. and Venter,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
            Rockville, MD, USA
COMMENT     This sequence was identified as CDM:10211866 by the submitter.
            For further information on this sequence e-mail to fly@celera.com.
            * NOTE: This is a 'working draft' sequence.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
FEATURES             Location/Qualifiers
     source          1. .31427
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BASE COUNT     8828 a   6834 c   6605 g   9160 t
ORIGIN


  Query Match             1.4%;  Score 20;  DB 43;  Length 31427;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    344 aagaagaagcagatgacggc 363
          ||||||||||||||||||||
Db   6506 AAGAAGAAGCAGATGACGGC 6487


RESULT   6
AC005052
LOCUS       AC005052   144734 bp    DNA             HTG       12-JUN-1998
DEFINITION  Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3
            unordered pieces.
ACCESSION   AC005052
VERSION     AC005052.1  GI:3212939
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 144734)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 144734)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUN-1998) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     * NOTE: This is a 'working draft' sequence. It currently
            * consists of 3 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1    12548: contig of 12548 bp in length
            *    12549    12565: gap of unknown length
            *    12566    66999: contig of 54434 bp in length
            *    67000    67016: gap of unknown length
            *    67017   144734: contig of 77718 bp in length.
FEATURES             Location/Qualifiers
     source          1. .144734
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="RG038K21"
BASE COUNT    37035 a  34072 c  33954 g  39639 t     34 others
ORIGIN


  Query Match             1.4%;  Score 20;  DB 33;  Length 144734;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    673 agcctgcccaacgaaagcta 692
          ||||||||||||||||||||
Db  84680 AGCCTGCCCAACGAAAGCTA 84699


RESULT   7
HTLV1RES
LOCUS       HTLV1RES     2153 bp    DNA             PRI       24-JUN-1998
DEFINITION  Human HTLV-I related endogenous retroviral sequence (HRES-1/1).
ACCESSION   X16660
VERSION     X16660.1  GI:3256208
KEYWORDS    endogenous retrovirus; long terminal repeat.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2153)
  AUTHORS   Perl,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-AUG-1989) Perl A., Roswell Park Memorial Institute,
            666 Elm Street, Buffalo, NY 14263, USA
  REMARK    revised by [3]
REFERENCE   2  (bases 1 to 2153)
  AUTHORS   Perl,A., Rosenblatt,J.D., Chen,I.S., DiVincenzo,J.P., Bever,R.,
            Poiesz,B.J. and Abraham,G.N.
  TITLE     Detection and cloning of new HTLV-related endogenous sequences in
            man
  JOURNAL   Nucleic Acids Res. 17 (17), 6841-6854 (1989)
  MEDLINE   89386040
REFERENCE   3  (bases 1 to 2153)
  AUTHORS   Perl,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUN-1998) Perl A., Roswell Park Memorial Institute,
            666 Elm Street, Buffalo, NY 14263, USA
COMMENT     On Jun 26, 1998 this sequence version replaced gi:38034.
            Data kindly reviewed (08-JAN-1990) by Perl A.
FEATURES             Location/Qualifiers
     source          1. .2153
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /cell_type="T lymphocyte"
                     /cell_line="MA-T"
                     /clone_lib="lambda DASH"
                     /clone="HRES-1/1"
     LTR             310. .994
                     /note="putative retroviral"
     repeat_unit     310. .313
                     /note="A"
                     /rpt_type=INVERTED
     misc_feature    463. .470
                     /note="TAR sequence (trans-activation region)"
     TATA_signal     782. .788
     misc_feature    839. .844
                     /note="putative"
     repeat_unit     990. .993
                     /note="A"
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                     /rpt_type=INVERTED
     misc_binding    998. .1015
                     /bound_moiety="tRNA primer"
     gene            1146. .1817
                     /gene="p25"
     CDS             1146. .1817
                     /gene="p25"
                     /codon_start=1
                     /product="p25 protein"
                     /protein_id="CAA34646.1"
                     /db_xref="GI:38035"
                     /db_xref="SPTREMBL:P13985"
                     /translation="MRCAHAPAPRTRYPTRAPSGPRPPSRSQAQTPPRSVPRLRPRHR
                     HPQDPRSPGPAPRHRRPPRPDPRAPPARASYRRFRTWPSATSWERRRLSPGHRALARG
                     PPARLGGEGPGAGDRRREGPDRSPRQPPVLPAAAAQPDSSSAQAPGPSTLRPAATARR
                     KRRWATRGPAHPAFARAHGEAGAGRVRTSARAGSTCAGWALWRCALRWAERQVGALGA
                     ESRFP"
     gene            1385. .1801
                     /gene="p15"
     CDS             1385. .1801
                     /gene="p15"
                     /codon_start=1
                     /product="p15 protein"
                     /protein_id="CAA34647.1"
                     /db_xref="GI:38036"
                     /db_xref="SPTREMBL:P13986"
                     /translation="MAVCDILGAAPPLAGSPCTRPRSAGASRWGRTWGGGPEEGGARP
                     VPTATAGPPSGCGPAGLQLRAGARALHPPSGRDREEEEEMGYARPGPPRVRACARGGR
                     GGAREDFGARRKHVRGLGALAVCAEVGRAAGGGVGG"
BASE COUNT      510 a    626 c    609 g    408 t
ORIGIN


  Query Match             1.4%;  Score 19;  DB 10;  Length 2153;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     220 gccccccgccccgcgcaccc 238
           ||||||||||||||||||||
Db    1161 GCCCCCGCCCCGCGCACCC 1179


RESULT  8
AF072440/c
LOCUS       AF072440     4316 bp    DNA             BCT       30-OCT-1998
DEFINITION  Enterobacter gergoviae GTPase (bipA) gene, partial cds; glutamine
            synthetase (glnA) and nitrogen regulatory protein (ntrB) genes,
            complete cds; and nitrogen regulatory protein (ntrC) gene, partial
            cds.
ACCESSION   AF072440
VERSION     AF072440.1  GI:3808289
KEYWORDS    .
SOURCE      Enterobacter gergoviae.
  ORGANISM  Enterobacter gergoviae
            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
            Enterobacter.
REFERENCE   1  (bases 1 to 4316)
  AUTHORS   Dong,Y.M. and Li,J.D.
  TITLE     The cloning of glnA, ntrB, and ntrC from Enterobacter gergoviae
            57-7 and their characterization
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 4316)
  AUTHORS   Dong,Y.M. and Li,J.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JUN-1998) Cell and Gene-Engineering, Institute of
            Botany, Chinese Academy of Sciences, Nanxincun 20, Xiangshan,
            Beijing 100093, P.R. China
REFERENCE   3  (bases 1 to 4316)
  AUTHORS   Dong,Y.M. and Li,J.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-OCT-1998) Cell and Gene-Engineering, Institute of
            Botany, Chinese Academy of Sciences, Nanxincun 20, Xiangshan,
            Beijing 100093, P.R. China
  REMARK    Nucleotide and amino acid sequences updated by submitter
COMMENT     On Oct 30, 1998 this sequence version replaced gi:3288877.
FEATURES             Location/Qualifiers
     source          1. .4316
                     /organism="Enterobacter gergoviae"
                     /strain="57-7"
                     /db_xref="taxon:61647"
     gene            complement(<1. .359)
                     /gene="bipA"
     CDS             complement(<1. .349)
                     /gene="bipA"
                     /codon_start=1
                     /transl_table=11
                     /product="GTPase"
                     /protein_id="AAC69322.1"
                     /db_xref="GI:3808292"
                     /translation="MIENLRNIAIIAHVDHGKTTLVDKLLQQSGTFDARTEAQERVMD
                     SNDLEKERGITILAKNTAIKWNDYRINIVDTPGHADFGGEVERVMSMVDSVLLVVDAF
                     DGPMPQTRFVTKKA"
     RBS             complement(357. .359)
                     /gene="bipA"
     gene            714. .2137
                     /gene="glnA"
     RBS             714. .719
                     /gene="glnA"
     CDS             728. .2137
                     /gene="glnA"
                     /EC_number="6.3.1.2"
                     /note="L-glutamate:ammonium ligase (ADP forming)"
                     /codon_start=1
                     /transl_table=11
                     /product="glutamine synthetase"
                     /protein_id="AAC69320.1"
                     /db_xref="GI:3808290"
                     /translation="MSAEHVLTMLNEHEVKFVDLRFTDTKGKEQHVTIPSHQVNAEFF
                     EEGKMFDGSSIGGWKGINESDMVLMPDASTAVIDPFYEEPTLIIRCDILEPGTLQGYD
                     RDPRSIAKRAEEYLRATGIADTVLFGPETEFFLFDDIRFGASISGSHVAIDDIEGAWN
                     SSTKYEGGNKGHRPGVKGGYFPVPPVDSSQDIRSTMCMIMEEMGLVVEAHHHEVATAG
                     QNEVATRFNTMTKKADEIQIYKYVVHNVAHRFGKTATFMPKPMFGDNGSGMHCHMSLA
                     KNGTNLFSGDKYAGLSEQALFYIGGVIKHAKAINALANPTTNSYKRLVPGYEAPVMLA
                     YSARNRSASIRIPVVTSPKARRIEVRFPDPAANPYLCFAALLMAGLDGIKNKIHPGEA
                     MDKNLYDLPPEEAKEIPQVAGSLEEALQALDADREFLTAGGVFTNDAIDAYIALRLEE
                     NDRVRMTPHPVEFELYYSV"
     gene            2313. .3375
                     /gene="ntrB"
     RBS             2313. .2318
                     /gene="ntrB"
     CDS             2326. .3375
                     /gene="ntrB"
                     /codon_start=1
                     /transl_table=11
                     /product="nitrogen regulatory protein"
                     /protein_id="AAC69321.1"
                     /db_xref="GI:3808291"
                     /translation="MATGTLPDAGQILNSLINSILLVDDDLAVHFANPAAQQLLAQSS
                     RKLFGTPLPELLSYFSLNIGLMQESLQAGQGFTDNEVTLVIDGRSHILSLTAQRLPEG
                     FILLEMAPMDNQRRLSQEQLQHAQQVAARDLVRGLAHEIKNPLGGLRGAAQLLSKALP
                     DPALTEYTKVIIEQADRLRNLVDRLLGPQHPGMHVTESIHKVAERVVKLVSMELPDNV
                     KLIRDYDPSLPELPHDPDQIEQVLLNIVRNALQALGPEGGEIVLRTRTAFQLTLHGVR
                     YRLAARIDVEDNGPGIPPHLQDTLFYPMVSGREGGTGLGLSIARSLIDQHSGKIEFTS
                     WPGHTEFSVYLPIRK"
     gene            3376. .>4316
                     /gene="ntrC"
     RBS             3376. .3381
                     /gene="ntrC"
     CDS             3384. .>4316
                     /gene="ntrC"
                     /codon_start=1
                     /transl_table=11
                     /product="nitrogen regulatory protein"
                     /protein_id="AAC69323.1"
                     /db_xref="GI:3808293"
                     /translation="MQRGIAWIVDDDSSIRWVLERALTGAGLSCTTFESGNEVLDALT
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                TKTPDVLLSDIRMPGMDGLALLKQIKQRHPMLPVIIMTAHSDLDAAVSAYQQGAFDYL
                PKPFDIDEAVALVDRAISHYQEQQQPRNAPISSPTADIIGEAPAMQDVFRIIGRLSRS
                SISVLINGESGTGKELVAHALHRHSPRSKAPFIALNMAAIPKDLIESELFGHEKGAFT
                GANTVRQGRFEQADGGTLFLDEIGDMPLDVQTRLLRVLADGQFYRVGGYAPVKVDVRI
                IAATHQNLEQRVQEGKFREDLFHRLNVIRRPAAKL"
BASE COUNT      994 a   1199 c   1150 g    973 t
ORIGIN


  Query Match             1.4%;  Score 19;  DB 2;  Length 4316;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1230 acagcaatccggtacgttc 1248
          ||||||||||||||||||
Db    272 ACAGCAATCCGGTACGTTC 254


RESULT  9
AF067430/c
LOCUS       AF067430     6417 bp    DNA             ROD       05-OCT-1999
DEFINITION  Mus musculus Smarcel-related protein (Smarcelr) gene, complete cds.
ACCESSION   AF067430
VERSION     AF067430.1  GI:4321967
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 6417)
  AUTHORS   Wattler,F., Wattler,S., Kelly,M., Skinner,H.B. and Nehls,M.
  TITLE     Cloning, chromosomal location, and expression analysis of murine
            Smarcel-related, a new member of the high-mobility 365 group gene
            family
  JOURNAL   Genomics 60 (2), 172-178 (1999)
  MEDLINE   99417677
REFERENCE   2  (bases 1 to 6417)
  AUTHORS   Wattler,S., Wattler,F. and Nehls,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-MAY-1998) New Technologies, Lexicon Genetics Inc.,
            4000 Research Forest Drive, The Woodlands, Texas 77381, USA
FEATURES             Location/Qualifiers
     source          1. .6417
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /chromosome="10"
                     /map="43 cM"
     mRNA            join(270. .337,555. .610,1256. .1364,1655. .1858,2128. .2295,
                     2128. .2295,2773. .2845,3225. .3440,3589. .3721,3804. .4230)
                     /gene="Smarcelr"
                     /product="Smarcel-related protein"
     gene            270. .4230
                     /gene="Smarcelr"
                     /note="similar to Mus musculus Baf57 and other Smarcel
                     genes"
     CDS             join(573. .610,1256. .1364,1655. .1858,2128. .2295,2773. .2845,
                     3225. .3440,3589. .3721,3804. .3816)
                     /gene="Smarcelr"
                     /note="contains HMG domain and kinesin-like coiled-coil
                     domain; SWI/SNF related, matrix associated, actin
                     dependent regulator of chromatin subfamily E, member
                     1-related protein"
                     /codon_start=1
                     /product="Smarcel-related protein"
                     /protein_id="AAD15897.1"
                     /db_xref="GI:4321968"
                     /translation="MSHGPRQPGAATAPAGGKTPGQHGAFVVAVKQERSEGSRAGEKG
                     PQEEEPVKKRGWPKGKKRKKILPNGPKAPVTGYVRFLNERREQIRTRHPDLPFPEITK
                     MLGAEWSKLQPAEKQRYLDEAEKEKQQYLKELWAYQQSEAYKVCTEKIQENKIKKEDS
                     SSGLMNTLLNGHKGVDCDGFSTFDVPIFTEEFLDQNKAREAELRRLRKMNVAFEEQNA
                     VLQRHTQSMSSARERLEQELALEERRTLALQQQLQAVRQALTASFASLPVPGTGETPT
                     LGTLDFYMARLHGAIERDPAQHERLIARVKEILARVASEHL"
     polyA_site      4209. .4214
                     /gene="Smarcelr"
BASE COUNT      1394 a   1863 c   1788 g   1372 t
ORIGIN


  Query Match             1.4%;  Score 19;  DB 12;  Length 6417;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    217 gcagcccccgccccgcgca 235
          ||||||||||||||||||
Db    382 GCAGCCCCCGCCCCGCGCA 364


RESULT  10
CELT14F9
LOCUS       CELT14F9    36679 bp    DNA             INV       04-MAR-1996
DEFINITION  Caenorhabditis elegans cosmid T14F9.
ACCESSION   U50199
VERSION     U50199.1  GI:1213552
KEYWORDS    .
SOURCE      Caenorhabditis elegans strain=Bristol N2.
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
            Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 36679)
  AUTHORS   Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
            Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
            Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
            Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
            Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
            Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
            O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
            Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
            Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
            Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
            Wilkinson-Sproat,J. and Wohldman,P.
  TITLE     2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
            elegans
  JOURNAL   Nature 368 (6466), 32-38 (1994)
  MEDLINE   94150718
REFERENCE   2  (bases 1 to 36679)
  AUTHORS   Miller,N and Langston,Y.
  TITLE     The sequence of C. elegans cosmid T14F9
  JOURNAL   Unpublished (1996)
REFERENCE   3  (bases 1 to 36679)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-FEB-1996) Robert Waterston
COMMENT                 Submitted by:
                        Genome Sequencing Center
                        Department of Genetics, Washington University,
                        St. Louis, MO  63110, USA, and
                        Sanger Centre, Hinxton Hall
                        Cambridge CB10 IRQ, England
                        e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
                        NEIGHBORING COSMID INFORMATION:
            The 5' cosmid is T24C12, 200 bp overlap;3' cosmid is F07D10, 200 bp
            overlap.  Actual start of this cosmid is at base position 197 of
            CELT14F9; actual end is at 36483 of CELT14F9
            The poly-G run from 8005 to 8024 may be off by one G. An exact
            number could not be determined.

            NOTES:
            Coding sequences below are predicted from computer analysis, using
            the program Genefinder(P. Green and L. Hillier, ms in preparation).
FEATURES             Location/Qualifiers
     source          1. .36679
                     /organism="Caenorhabditis elegans"
                     /strain="Bristol N2"
                     /db_xref="taxon:6239"
     repeat_region   8005. .8024
                     /note="Poly G run"
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gene            10617. .13085
                /gene="T14F9.4"
CDS             join(10617. .10736,10935. .11036,11092. .11265,12089. .12286,
                12342. .12929,12984. .13085)
                /gene="T14F9.4"
                /codon_start=1
                /evidence=not_experimental
                /protein_id="AAA91262.1"
                /db_xref="GI:1213553"
                /translation="MLGLEKPGSSDISSSSTDTSAISPISVSSMPLSPDKEKKKISFV
                RYNPDIPQIVTSFKGYQKLMYQGYRYNIYQIAPERNFKSWRCVCAKKMHDGQWCKCRA
                ETTMDNKNACTKGSHNHPPRHHVAEIEFIKSQLYSAALENPDHDAGDLVNQASMYLSD
                GVMFDNKESIKKSLVVARNKDGKPKKPRSKRMMKFEVDDDDENEYKMPKLETDISCFL
                PFINNMVKVEPPFSHTPTIQIPQPIPTPIQHQQQEQSNLLQPATLNGMNNPWMGMEDH
                LAMIWAANAMLNPGLDVLSTIAALSKHQQHVQGPSPQQAATAPTTASLSSNLSVSSFT
                PQMPKEASIAIPAPLQVLNLKDLKPLPPLANIQTSPVIQAANLLLPVAALKKDSSTQT
                TEEIKVSQCLTSGCGCRVIRICCCDEGVCRRTAAC"
gene            18470. .21495
                /gene="T14F9.3"
CDS             join(18470. .18568,18613. .18739,18793. .18918,18964. .19079,
                19421. .19633,19677. .19907,19952. .20127,20175. .20435,
                20477. .20599,21300. .21495)
                /gene="T14F9.3"
                /note="coded for by C. elegans cDNA yk79c7.3; coded for by
                C. elegans cDNA yk79c7.5;  Similar to beta-hexosaminidase
                beta subunit."
                /codon_start=1
                /protein_id="AAA91263.1"
                /db_xref="GI:1213554"
                /translation="MRLLIPILIFALITTAVTWFYGRDDPDRWSVGGVWPLPKKIVYG
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                DECPSGPPVHGASEEYLLRVSLTEAVINAQTVWGALRAMESLSHLVFYDHKSQEYQIR
                TVEIFDKPRFPVRGIMIDSSRHFLSVNVIKRQLEIMSMNKLNVLHWHLVDSESFPYTS
                VKFPELHGVGAYSPRHVYSREDIADVIAFARLRGIRVIPEFDLPGHTSSWRGRKGFLT
                ECFDEKGVETFLPNLVDPMNEANFDFISEFLEEVTETFPDQFLHLGGDEVSDYIVECW
                ERNKKIRKFMEEKGFGNDTVLLENYFFEKLYKIVENLKLKRKPIFWQEVFDNNIPDPN
                AVIHIWKGNTHEEIYEQVKNITSQNFPVIVSACWYLNYIKYGADWRDEIRGTAPSNSR
                YYYCDPTNFNGTVAQKELVWGGIAAIWGELVDNTNIEARLWPRASAAAERLWSPAEKT
                QRAEDAWPRMHELRCRLVSRGYRIQPNNNPDYCPFEFDEPPATKTEL"
tRNA            complement(22182. .22253)
                /note="Asp;  codon recognized: GAC"
gene            complement(24191. .24790)
                /gene="lin-32"
CDS             complement(join(24191. .24337,24722. .24790))
                /gene="lin-32"
                /note="T14F9.5"
                /codon_start=1
                /product="hlh transcription factor"
                /protein_id="AAA91264.1"
                /db_xref="GI:1213555"
                /translation="MRRSAANERERRRMNTLNVAYDELREVLPEIDSGKKLSKFETLQ
                MAQKYIECLSQILKQDSKNENLKSKSG"
gene            28980. .31448
                /gene="T14F9.2"
CDS             join(28980. .28988,29309. .29409,29462. .29866,29912. .30036,
                30082. .30254,30301. .30420,31194. .31448)
                /gene="T14F9.2"
                /codon_start=1
                /evidence=not_experimental
                /protein_id="AAA91265.1"
                /db_xref="GI:1213556"
                /translation="MTGMSEEDQSAPNGSVPGPDAKAWPELTVDLEPEVWRALYREKH
                GEKFRCSVEMLMELEEISCEIEAEQKLLDILVKVTFIERNLCLNGPQSGESLFESLEE
                ARSDEQPLLFATVSDLTSFCDSMKPIFQTEKVKGTLIYRNSGYQSRRFIQYIRRRLEP
                GDVIDSTTFRQVIQDFQETIGVPDSVKTFAKSELTLDFTSLRTVARNVPGFRYDKSLE
                RLDLTPEAEHHLPLHLPIFTETLDFNNPHKHDYSRVFSCYVRNDCTQYPNRLKGTVVS
                ETGLGIGFMCFQDNMKDYLGNDLEKGTFNAANYRFLAVEGNINPSNLYEQFEVFKVVN
                IPFGFDNNLVTTGNETIYRVHFNLEKVDSTFENVQTELEATLRRVVHRTRKSKEDNDN
                SDD"
gene            32897. .34887
                /gene="T14F9.1"
CDS             join(32897. .32977,33031. .33126,33181. .33321,33370. .33483,
                33533. .33640,33689. .34183,34448. .34650,34713. .34887)
                /gene="T14F9.1"
                /note="coded for by C. elegans cDNA yk89e9.5; coded for by
                C. elegans cDNA cm7g5; coded for by C. elegans cDNA
                cm14b9; coded for by C. elegans cDNA yk52g5.5; coded for
                by C. elegans cDNA yk76e5.5; coded for by C. elegans cDNA
                yk131f11.5; coded for by C. elegans cDNA yk87d8.5; coded
                for by C. elegans cDNA yk76e5.3; coded for by C. elegans
                cDNA CEESU78FB; coded for by C. elegans cDNA yk87d8.3;
                coded for by C. elegans cDNA yk52g5.3; coded for by C.
                elegans cDNA yk131f11.3;  similar to S. cerevisiae
                vacuolar H(+)-ATPase 54 kd subunit (SP:P41807)"
                /codon_start=1
                /protein_id="AAA91266.1"
                /db_xref="GI:1213557"
                /translation="MAEVPHHNIPAVDMLNATSRLQLEAQELRNNKPNWGSYFRSQMI
                QEDDYNFITSFENAKSKEERDQVLAANNANGQAAKTMANLITQVAKDQNVRYVLTLFD
                DMLQEDKSRVELFHSAAARQKRTVWSQYLGILQRQDNFIVNQMSSIIAKLACFGTTRM
                EGQDLQYYFSFLKEQLKNSTTNDYMNTTARCLQMMLRHDEYRHEFVDSDGVQTLVTAL
                NGKTNFQLQYQLIFAVWCLTFNADIARKAPSLGLIQALGDILSESTKEKVIRIILASF
                VNILSKVDEREVKREAALQMVQCKTLKTLELMDAKKYDDPDLEDDVKFLTEELTLSVH
                DLSSYDEYYSEVRSGRLQWSPVHKSEKFWRENASKFNDKQFEVVKILIKLLESSHDPL
                ILCVASHDIGEYVRHYPRGKTVVEQYQGKAAVMRLLTAEDPNVRYHALLAVQKLMVHN
                WEYLGKQLDSDVQTDTVAVK"
BASE COUNT    11140 a   7051 c   6678 g  11810 t
ORIGIN

  Query Match             1.4%;  Score 19;  DB 34;  Length 36679;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     619 cccttcggctttgacaaca 637
           ||||||||||||||||||||
Db   31266 CCCTTCGGCTTTGACAACA 31284


RESULT  11
SPBC2F12
LOCUS       SPBC2F12     38012 bp    DNA                 PLN       23-NOV-1999
DEFINITION  S.pombe chromosome II cosmid c2F12.
ACCESSION   Z97211
VERSION     Z97211.2  GI:6273683
KEYWORDS    60s ribosomal protein L22; atf creb-family transcription factor;
            byr2; bZIP; bZIP transcription factor; ceg1; cell cycle regulation;
            ergosterol synthesis; Homol D box; Homol E box; IMP dehydrogenase;
            inosine-5'-monophosphate dehydrogenase; kinesin-like; L2; L8;
            leucine zipper; mitochondrial 60s ribosomal protein L17; mitotic
            cell cycle start; mrna capping enzyme; mrna guanylyltransferase;
            rep2; rpk37; rpk5b; rpk5c; rpl17; rpl8-2; serine rich; serine
            threonine protein kinase; transcriptional activator; zinc finger
            C2H2 type.
SOURCE      fission yeast.
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
            Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE   1  (bases 1 to 38012)
  AUTHORS   Wood,V., Rajandream,M.A., Barrell,B.G., Skelton,J. and
            Churcher,C.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JUN-1997) European Schizosaccharomyces genome
            sequencing project, Sanger Centre, The Wellcome Trust Genome
            Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk
            and The Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA
COMMENT     On Nov 7, 1999 this sequence version replaced gi:2239231.
            Notes:
            Details of yeast sequencing at the Sanger Centre are available on
            the World Wide Web.
            (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
            During 1995 to 1996 about 80% of S. pombe chromosome 1 was
            sequenced by the Sanger Centre.  The sequencing of the S. pombe
            genome is now being continued with funding from The European
            Commission. Fourteen European sequencing laboratories, including
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the Sanger Centre, are participating in the project.
Protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in PomBase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program Sp3splice. CAUTION: It is possible that for any individual CDS we may have underestimated or overestimated the number of introns/exons or we may not have chosen the correct splice donor/acceptor sites.
CDS are numbered using the following system eg SPBC25H2.01c. SP (S. pombe), B (chromosome 2), c25H2 (cosmid name), .01 (first CDS), c (complementary strand).
The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.
The length in codons is given for each CDS.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
Cosmid c2F12 is overlapped at the 5' end by cosmid c19C2 and at the 3' end by cosmid c1D7 .

FEATURES Location/Qualifiers

source 1. .38012
/organism="Schizosaccharomyces pombe"
/strain="972h-"
/db_xref="taxon:4896"
/chromosome="II"
/clone="cosmid c2F12"
/map="IIR"

misc_feature 1. .789
/note="nominal overlap with cosmid SPBC19C2, EM:AL109731 S.pombe chromosome 2"

gene complement(1. .371)
/gene="SPBC2F12.16"

CDS complement(join(1. .308,359. .371))
/partial
/gene="SPBC2F12.16"
/note="SPBC2F12.16, similarity: to C elegans O17040,T15B7.2 PROTEIN, (271 aa), fasta scores, opt:135, E():2.7e-06, (36 .8% identity in 87 aa overlap)"
/codon_start=1
/label=SPBC2F12.16
/product="hypothetical protein"
/protein_id="CAB10163.2"
/db_xref="GI:6448602"
/db_xref="SWISS-PROT:O14346"
/translation="MSKILKIQYLKLYNVISCFLWMSVLLRTGLIWGITKDTAVVFHE TNTLVRWVQTLAIAEVFHSIFGLVSSSPLTTIIQVASRLYLVWGVCYPFSYVIEGSPI YLSMI"

misc_feature complement(309. .327)
/gene="SPBC2F12.16"
/note="ttaacaaagttaaaaatag, splice branch and acceptor"

misc_feature complement(353. .358)
/gene="SPBC2F12.16"
/note="gtaaga, splice donor sequence"

gene 1008. .2069
/gene="SPBC2F12.15c"

CDS join(1008. .1235,1308. .2069)
/gene="SPBC2F12.15c"
/note="SPBC2F12.15c, len:329aa; similarity: to YNL326C, YN6 6_YEAST, P42836, hypothetical 39.2 kd protein, (336aa), fas ta scores, opt:340, E():2.7e-1, (33.2% identity in 217 aa o verlap)"
/codon_start=1
/label=SPBC2F12.15c
/product="hypothetical protein"
/protein_id="CAB10162.1"
/db_xref="GI:2239244"
/db_xref="SWISS-PROT:O14345"
/translation="MNLIHKVSTICQCVLVILAKYCMQIIALSLMSGVQWLAWGIYKI NKNRVGIIILFLYIMIVTCYVLTNLTPPGSPSETSFDPNSTRQYMTLQNGKSRFCEKC QEYKCDRSHHCSQCNKCILRMDHHCMWFKNCVGFRNHKFFFLECFYLNLYSICVLYST FVAITKTFTAEGANISAIYLVFWGFLFAFAVGMSIVMTAFTFYHTSLLIHNLSTLESM SSSWSRYTHSTQPFNVGWYENWCQIMGKSPFLWLLPFPNSIGEGVEYPLNANALPYLP QTEEKNDKLYKSSVPASIAGAEGWSSDEEQYAMKNRRWNPHMGQYEWIEDFLV"

misc_feature 1236. .1241
/gene="SPBC2F12.15c"
/note="gtacgt, splice donor sequence"

misc_feature 1290. .1307
/gene="SPBC2F12.15c"
/note="ctaactcttctgtttcag, splice branch and acceptor"

gene 3582. .5488
/gene="SPBC2F12.14c"

CDS join(3582. .4038,4371. .5488)
/gene="SPBC2F12.14c"
/note="SPBC2F12.14c, len:524aa, similarity: to IMH2_YEAST, P50095, probable inosine-5'-monophosphate dehydrogenase (52 3aa), fasta scores, opt:2200, E():0, (62.8% identity in 524 aa overlap)"
/codon_start=1
/label=SPBC2F12.14c
/product="probable inosine-5'-monophosphate dehydrogenase"
/protein_id="CAB10161.1"
/db_xref="GI:2239243"
/db_xref="SPTREMBL:O14344"
/translation="MSAFKPYTEALEVLKKYEKKDGLSIDDLIRHNFQGGLTFNDFLI LPGYIDFVPNNVSLETRISRNIVLKTPFMSSPMDTVTEDQMAIYMALLGGIGVIHHNC TPEEQAAMVRKVKKYENGFILDPVVFSPQHTVGDVLKIKETKGFSGIPITENGKLRGK LVGIVTSRDVQFHKDTNTPVTEVMTPREELITTAEGISLERANEMLRKSKKGKLPVVD KDDNLVALLSLTDLMKNLHFPLASKTSDTKQLMVAAAIGTRDDDRTRLALLAEAGLDA VVIDSSQGNSCFQIEMIKWIKKTYPKIDVIAGNVVTREQTASLIAAGADGLRVGMGSG SACITQEVMACGRPQATAIAQVAEFASQFGIGVIADGGIQNVGHMVKSLSLGATAVMM GGLLAGTTESPGEYYVREGQRYKSYRGMGSIAAMEGTGVNKNASTGRYFSENDAVRVA QGVSGLVVDKGSLLRFLPYLYTGLQHALQDIGTKSLDELHEAVDKHEVRFELRSSAAI REGDIQGFATYEKRLY"

misc_feature join(3951. .4038,4371. .4429)
/gene="SPBC2F12.14c"
/note="Match to PF00571 CBS, CBS domain Score 26.72"

intron 4039. .4370
/gene="SPBC2F12.14c"
/note="confirmed intron"

misc_feature 4039. .4044
/gene="SPBC2F12.14c"
/note="gtaagt, splice donor sequence"

misc_RNA 4208. .4288
/gene="SPBC2F12.14c"
/note="putative snoRNA Sp-snR54, complements: Sp-18S-rRNA and modifies Am989. Yeast snR54 homolog. (Todd Lowe)"

misc_feature 4360. .4370
/gene="SPBC2F12.14c"
/note="ctaacctttag, splice branch and acceptor"

misc_feature 4463. .4621
/gene="SPBC2F12.14c"
/note="Match to PF00571 CBS, CBS domain Score 46.07"

misc_feature 4715. .5380
/gene="SPBC2F12.14c"
/note="Match to PF00478 IMPDH_C, IMP dehydrogenase / GMP reductase C terminus Score 363.99"

gene complement(5821. .8528)
/gene="SPBC2F12.13"

CDS complement(join(5821. .8441,8498. .8528))
/gene="SPBC2F12.13"
/note="SPBC2F12.13, len:883aa; similarity: to YGL216W, YGW6 _YEAST, P53086, putative kinesin-like protein, (805aa), fas ta scores, opt:1347, E():0,(39.0% identity in 731 aa overla p)"
/codon_start=1
/label=SPBC2F12.13
/product="kinesin-like protein"
/protein_id="CAB10160.1"
/db_xref="GI:2239242"
/db_xref="SWISS-PROT:O14343"
/translation="MSRQSSITVTVRVRPFSTAESANLIASSDRLSFGTSSSLRNPGS GRQIRRVVKVLDGRVLVFDPPDETTATLSATNRRLSTSQQSLARLSRKSNNSAGFGRD LRYAFDRVFDETATQQQVYERTARPLLDNILDGFNATIFAYGATGCGKTHTISGTMQD PGLIYLTLKELFERMDHLRDEKIFDLRLSYLEIYNETIRDLLVSPTPNQAKPLNLRED ADRRITVPGLTSLSPESLEEIIDIIMKGNANRTMSPTEANAASSRSHAVLQVTLIQKP

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                     RTAGINEDHTLATLSIIDLAGSERATATKLRGSRLFEGANINKSLLALGNCINALCDP
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                     EVLRNMISVDRHVSQYVKAIVELREQISELENRLAQIDLSSQSNGSDQDAVTQSFAHE
                     SKLAEARNLLRMTFEETLPLQNDTINKVEKVKHFDDSIRVLKYWLSCYERILPNSADE
                     RVFLVRSKLESLLTRRAEIIADIDPELVYQKFQRSVSHIINTYKQEGATMYADVLQDE
                     VDLLKSIIENQVLDAQNKVDEFTPVLESLLRSSFKASSLLKEGGMQELFSILEKWLLG
                     IGLGEKPNISVLSESYKLNSTSDDSRTINRDRVHSFPTQPLLNNNLPRMFFVKSPKKP
                     VVFSKRSPKKRVRFDDSMSTSDSGASAYNSPIQTSKLKNMNFFNTMHMPSTPAHKRPE
                     NKNQIDVEINLTSPVSPMLEDKPEPGLLIKSPLEKKQEVNSESTQLDQLLAEDSSTDD
                     VSLPHLDTIDLDGSPVPKVPDLNFSRANMDSPTFILNNEAIHNFDFSKPKTRQSLSSL
                     TTLHLSNPANIIRKSLSMAENEEEKAT"
     misc_feature    complement(7219. .8163)
                     /gene="SPBC2F12.13"
                     /note="Match to PF00225 kinesin, Kinesin motor domain
                     Score 362.06"
     misc_feature    complement(8020. .8043)
                     /gene="SPBC2F12.13"
                     /note="PS00017 ATP/GTP-binding site motif A (P-loop)"
     misc_feature    complement(8442. .8455)

  Query Match              1.4%;  Score 19;  DB 8;  Length 38012;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1197 atcatccaaaacagatgaa 1215
           ||||||||||||||||||
Db    8555 ATCATCCAAAACAGATGAA 8573


RESULT  12
AB016875/c
LOCUS       AB016875     60476 bp    DNA              PLN       20-NOV-1999
DEFINITION  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9D7,
            complete sequence.
ACCESSION   AB016875
VERSION     AB016875.1  GI:3449316
KEYWORDS    HTG.
SOURCE      Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui TAC
            clone:K9D7.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
            eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
            Arabidopsis.
REFERENCE   1  (sites)
  AUTHORS   Nakamura,Y.
  TITLE     Structural Analysis of Arabidopsis thaliana Chromosome 5. VIII
  JOURNAL   Unpublished (1998)
REFERENCE   2  (bases 1 to 60476)
  AUTHORS   Nakamura,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-AUG-1998) to the DDBJ/EMBL/GenBank databases.
            Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of
            Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan
            (E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935,
            Fax:+81-438-52-3934)
FEATURES             Location/Qualifiers
     source          1. .60476
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia"
                     /db_xref="taxon:3702"
                     /chromosome="5"
                     /clone="K9D7"
                     /clone_lib="Mitsui TAC"
BASE COUNT    19833 a   9701 c  10325 g  20617 t
ORIGIN


  Query Match              1.4%;  Score 19;  DB 7;  Length 60476;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1037 tcctcagcctcgacggcgg 1055
           ||||||||||||||||||||
Db   35339 TCCTCAGCCTCGACGGCGG 35321


RESULT  13
AC002415
LOCUS       AC002415     93419 bp    DNA              HTG       12-AUG-1997
DEFINITION  Homo sapiens chromosome X clone bWXD142, *** SEQUENCING IN PROGRESS
            ***, 6 unordered pieces.
ACCESSION   AC002415
VERSION     AC002415.1  GI:2323256
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 93419)
  AUTHORS   Chen,E., Brownstein,B.H., States,D.J., Schlessinger,D. and
            Mazzarella,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished (1997)
REFERENCE   2  (bases 1 to 93419)
  AUTHORS   Brownstein,B.H., States,D.J. and Mazzarella,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-AUG-1997) Center for Genetics in Medicine, Box 8232,
            Washington University School of Medicine, 4566 Scott Avenue, St.
            Louis, MO 63110, USA
COMMENT     Current status of this project is available at:
            'http://genome.wustl.edu/cgm/seq_projects.html'
            Submitted by:
            Ellson Chen,
            Advanced Center for Genetic Technology,
            Applied Biosystems Division of Perlin Elmer Corp.,
            850 Lincoln Center Drive,
            Foster City, CA 94404 USA
            e-mail: ellson@genseq.apldbio.com

            and

            Buddy Brownstein,
            Center for Genetics in Medicine,
            Washington University School of Medicine, Box 8232
            4566 Scott Avenue,
            St. Louis, MO 63110, USA
            e-mail: buddy@genetics.wustl.edu

            and

            David J. States,
            Institute for Biomedical Computing
            Washington University in St. Louis
            700 South Euclid Ave.
            St. Louis, MO 63108 USA
            e-mail: states@ibc.wustl.edu.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 6 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     9560: contig of 9560 bp in length
            *     9561    25127: contig of 15567 bp in length
            *    25128    45675: contig of 20548 bp in length
            *    45676    73399: contig of 27724 bp in length
            *    73400    82075: contig of 8676 bp in length
            *    82076    93419: contig of 11344 bp in length.
FEATURES             Location/Qualifiers
     source          1. .93419
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="bWXD142"
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                     /chromosome="X"
BASE COUNT    25991 a  21189 c  20209 g  26030 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    810 attcatgggcatctccttt 828
          ||||||||||||||||||||
Db   4421 ATTCATGGGCATCTCCTTT 4439


RESULT  14
MUSTHREX17/c
LOCUS       MUSTHREX17    247 bp    DNA             ROD       18-OCT-1994
DEFINITION  Mouse thrombospondin (THBS1) gene, exon 17.
ACCESSION   M62465 S79284
VERSION     M62465.1  GI:202015
KEYWORDS    glycoprotein; thrombospondin.
SEGMENT     17 of 22
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) DNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Lawler,J., Duquette,M., Ferro,P., Copeland,N.G., Gilbert,D.J. and
            Jenkins,N.A.
  TITLE     Characterization of the murine thrombospondin gene
  JOURNAL   Genomics 11 (3), 587-600 (1991)
  MEDLINE   92128941
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Mus musculus"
                     /strain="BALB/c"
                     /sub_species="domesticus"
                     /db_xref="taxon:10090"
     intron          <1. .6
                     /gene="THBS1"
                     /number=16
     exon            7. .241
                     /gene="THBS1"
                     /number=17
     intron          242. .>247
                     /gene="THBS1"
                     /number=17
BASE COUNT       73 a     64 c     64 g     46 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    817 ggcatctcctttgccatc 834
          ||||||||||||||||||
Db    153 GGCATCTCCTTTGCCATC 136


RESULT  15
G14673/c
LOCUS       G14673        400 bp    DNA             STS       04-JAN-1996
DEFINITION  human STS SHGC-11830.
ACCESSION   G14673
VERSION     G14673.1  GI:1130412
KEYWORDS    STS sequence; primer; sequence tagged site.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
            Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 400)
  AUTHORS   Myers,R.M.
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Richard M. Myers
            Stanford Human Genome Center (SHGC)
            Stanford University School of Medicine
            Department of Genetics, M-344, Stanford, CA 94305, USA
            Tel: 4157259687
            Fax: 4157259689
            Email: myers@shgc.stanford.edu

            Primer A: CTAAGGAAAACCATTGTCAGCC
            Primer B: GTCTCAATTGTTGACGCTTATCC
            STS size: 131
            PCR Profile:
                  Initial incubation: 94 degrees C for 90 seconds

                  Denaturation:       94 degrees C for 15 seconds
                  Annealing:          62 degrees C for 23 seconds
                  Polymerization:     72 degrees C for 30 seconds
                  PCR Cycles:         30
                  Thermal Cycler:     Perkin Elmer 9600
            Protocol:
                  Template:       25 ng
                  Primer:         each 1 uM
                  dNTPs:          each 200 uM
                  Taq Polymerase: 0.05 units/ul
                  Total Vol:      10 ul

            Buffer:
                  MgCl2:          2.5 mM
                  KCl:            50  mM
                  Tris-HCl:       20  mM
                  pH:             8.3

            Prepared with primer pairs derived from T62818--Merck/UniEST.
FEATURES             Location/Qualifiers
     source          1. .400
                     /organism="Homo sapiens"
     STS             121. .251
     primer_bind     121. .142
     primer_bind     complement(229. .251)
BASE COUNT      113 a     85 c     88 g    114 t
ORIGIN


  Query Match             1.3%;  Score 18;  DB 13;  Length 400;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1266 cattacccttcagacaca 1283
          ||||||||||||||||||
Db    357 CATTACCCTTCAGACACA 340


Search completed: April 14, 2000, 18:33:06
Job time: 8214 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 14, 2000, 18:29:32 ; Search time 121.06 Seconds
(without alignments)
2883.016 Million cell updates/sec

Title: US-09-388-090-3
Perfect score: 1395
Sequence: 1 gtgttcaaaaaataccaata.....tcagggcaagtccccgtcaa 1395

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 311585 seqs, 125096042 residues

Word size : 0

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	1.3	965	1	X13598	Enterococcus faeca
	2	18	1.3	9960	1	V58939	Mycobacterium smeg
	3	18	1.3	10095	1	V58938	Mycobacterium tube
	4	17	1.2	196	1	T19263	Human gene signatu
c	5	17	1.2	229	1	V31989	BS106 polynucleoti
c	6	17	1.2	308	1	V31990	BS106 polynucleoti
c	7	17	1.2	482	1	V31992	BS106 polynucleoti
c	8	17	1.2	489	1	X00704	Human secreted pro
c	9	17	1.2	489	1	X00644	Human secreted pro
c	10	17	1.2	553	1	V31993	BS106 polynucleoti
	11	17	1.2	732	1	V29521	Homo sapiens LexA-
c	12	17	1.2	1029	1	V28875	Candida antartica
c	13	17	1.2	1348	1	V84576	Human secreted pro
	14	17	1.2	1503	1	V29523	Homo sapiens PSP1
	15	17	1.2	1787	1	V29522	Homo sapiens PSP1
	16	17	1.2	1803	1	V24135	Homo sapiens BAP28
	17	17	1.2	1835	1	V29524	Homo sapiens PSP1
	18	17	1.2	2040	1	V08860	Human cancer-relat
	19	17	1.2	2144	1	V29538	Homo sapiens PSP1-
	20	17	1.2	2187	1	V29535	Homo sapiens PSP1
	21	17	1.2	2187	1	V29536	Homo sapiens PSP1-
	22	17	1.2	2187	1	V29539	Homo sapiens PSP1-
	23	17	1.2	2551	1	V29537	Homo sapiens PSP1-
c	24	17	1.2	49377	1	V05287	The soraphen biosy
c	25	16	1.1	334	1	V75215	Staphylococcus aur
c	26	16	1.1	388	1	Q99376	Rat allograft infl
	27	16	1.1	588	1	X07117	Staphylococcus aur
c	28	16	1.1	894	1	T40228	Mutant farnesyldip
	29	16	1.1	918	1	T38731	Papaya ringspot vi
	30	16	1.1	926	1	X40028	Prostate cancer as
	31	16	1.1	929	1	T38329	Coat protein gene
c	32	16	1.1	1080	1	X14364	H. pylori GHPO 376
	33	16	1.1	1148	1	T71230	Papaya ringspot vi
	34	16	1.1	1158	1	T34672	Coat protein gene
	35	16	1.1	1288	1	Q36841	Cyclophilin C. Cyc
c	36	16	1.1	1479	1	T77329	Class II EPSPS DNA
c	37	16	1.1	1479	1	T93796	Class II EPSP synt
c	38	16	1.1	1479	1	V58021	Dichelobacter nodo
	39	16	1.1	2061	1	Q77669	Variant cyclomalto
	40	16	1.1	2157	1	Q25801	H13 gene. Human re
	41	16	1.1	2157	1	Q54772	Full-length human
	42	16	1.1	2157	1	V59844	Human retroviral r
	43	16	1.1	3710	1	V74716	Staphylococcus aur
	44	16	1.1	4190	1	V34854	Human retinal dege
c	45	16	1.1	4426	1	V09064	Bovine cGMP-bindin
c	46	16	1.1	4474	1	Q79703	Cyclic guanosine m
c	47	16	1.1	4841	1	T05696	Flax rust resistan
	48	16	1.1	4968	1	X20597	Polynucleotide seq
c	49	16	1.1	5541	1	Q55755	Escherichia coli g
	50	16	1.1	7900	1	X13068	Enterococcus faeca
c	51	16	1.1	8378	1	Q25811	Drosophila SLIT pr
	52	16	1.1	9432	1	Q99312	LKP1 operon. Haemo
	53	16	1.1	10461	1	X20553	Polynucleotide seq
	54	16	1.1	11907	1	Q45339	cDNA encoding htrx
c	55	16	1.1	13256	1	X20528	Polynucleotide seq
	56	16	1.1	13811	1	X20649	Polynucleotide seq
	57	16	1.1	14255	1	Q43526	ALL-1 gene cDNA. D
	58	16	1.1	14255	1	Q75181	ALL-1 (acute lymph
	59	16	1.1	14255	1	V20477	Human ALL-1/AF-4 o
	60	16	1.1	52297	1	T51411	Mycobacteriophage
	61	16	1.1	52298	1	Q47357	L5 mycobacteriopha
	62	15	1.1	47	1	V45614	Primer for Mycobac
	63	15	1.1	54	1	V70987	Primer 5'PKAc used
c	64	15	1.1	247	1	X11700	Human biallelic po
c	65	15	1.1	247	1	X11701	Human biallelic po
c	66	15	1.1	247	1	X12866	Human biallelic po
c	67	15	1.1	288	1	X41498	Human secreted pro
	68	15	1.1	307	1	T00043	Hepatitis GB virus
c	69	15	1.1	345	1	T60544	(Pro23-Lys37delAsn
c	70	15	1.1	383	1	X39585	Human secreted pro
c	71	15	1.1	409	1	V75474	Staphylococcus aur
c	72	15	1.1	417	1	T60542	MetGDNF degenerate
	73	15	1.1	438	1	T67431	H. pylori secreted
	74	15	1.1	448	1	V38433	cDNA encoding the
	75	15	1.1	493	1	Q59843	Human brain Expres
c	76	15	1.1	550	1	V63932	Mycobacterium tube
	77	15	1.1	570	1	Q27166	Mink growth hormon
	78	15	1.1	573	1	Q36018	Gene for mink Grow
	79	15	1.1	579	1	X23714	Pig growth hormone
	80	15	1.1	597	1	X23715	Pig growth hormone
	81	15	1.1	622	1	T98746	DNA encoding a S.
c	82	15	1.1	642	1	V23478	Pseudomonas XcpP s
	83	15	1.1	662	1	T83942	DNA encoding a Sta
	84	15	1.1	662	1	V53386	DNA encoding a sin
	85	15	1.1	766	1	X23719	Pig growth hormone
	86	15	1.1	795	1	T00051	Hepatitis GB virus
	87	15	1.1	804	1	T70089	DNA encoding inter
	88	15	1.1	807	1	X02185	E. coli dsbG DNA.
	89	15	1.1	811	1	Q22605	Mink pre-growth ho
c	90	15	1.1	865	1	V58741	Insertion sequence
	91	15	1.1	1000	1	V27350	Streptococcus pneu
	92	15	1.1	1074	1	X23720	Pig growth hormone
c	93	15	1.1	1102	1	X12946	Enterococcus faeca
c	94	15	1.1	1126	1	V58744	Insertion sequence
	95	15	1.1	1139	1	V08813	Gene No. 3 encodin
	96	15	1.1	1290	1	T67838	H. pylori secreted
	97	15	1.1	1290	1	X30416	H. pylori cell env
	98	15	1.1	1308	1	Q14367	Citrate synthase g
	99	15	1.1	1341	1	V29071	Mycobacterium tube
c	100	15	1.1	1367	1	X51727	DNA encoding a hum
	101	15	1.1	1371	1	T29383	Hamster flank orga
c	102	15	1.1	1434	1	T72221	Grapevine leafroll
	103	15	1.1	1438	1	X23317	Human 1-alpha-OHas
	104	15	1.1	1482	1	Q05236	Glucose-6-phosphat
c	105	15	1.1	1650	1	T04376	Moraxella catarrha
c	106	15	1.1	1662	1	T62457	Streptomyces venez

c 107	15	1.1	1700	1	T90097	Mch4 coding sequen
c 108	15	1.1	1704	1	V18819	Human protease FMH
c 109	15	1.1	1763	1	T36360	Bst DNA polymerase
c 110	15	1.1	1764	1	T90819	Bacillus stearothe
111	15	1.1	1767	1	Q98669	Sequence encoding
c 112	15	1.1	1770	1	T90820	B. stearothermophi
113	15	1.1	1788	1	V71036	mPKAc-green floure
114	15	1.1	1938	1	Q31987	Heat stable hydant
c 115	15	1.1	1946	1	V80304	Human GILR protein
116	15	1.1	1966	1	X04340	Human secreted pro
c 117	15	1.1	1988	1	Q20590	Sequence of native
118	15	1.1	2019	1	T15007	Type III (alpha-ty
c 119	15	1.1	2021	1	Q79725	Human L5/3 tumour
c 120	15	1.1	2021	1	T62438	Human L5/3 partial
121	15	1.1	2042	1	T59913	Yeast transcriptio
c 122	15	1.1	2060	1	V44862	Clone BV291_3 codi
c 123	15	1.1	2082	1	V41257	Mouse neuronal PAS
124	15	1.1	2092	1	T14529	Human adenylyl cyc
c 125	15	1.1	2100	1	V82073	DNA encoding gidA1
c 126	15	1.1	2116	1	T99541	Human hyaluronan s
c 127	15	1.1	2117	1	T96713	Human hyaluronate
c 128	15	1.1	2152	1	V26613	Human LICE3 cDNA.
129	15	1.1	2161	1	Q98671	Sequence encoding
c 130	15	1.1	2180	1	Q20589	Sequence of PCR-ge
c 131	15	1.1	2213	1	T47149	Macrophage stimula
c 132	15	1.1	2216	1	T47145	Macrophage stimula
c 133	15	1.1	2216	1	V72083	Human MSP cDNA. Tr
c 134	15	1.1	2219	1	Q79723	Human L5/3 tumour
c 135	15	1.1	2219	1	Q79724	Human L5/3 tumour
c 136	15	1.1	2219	1	T62437	Human L5/3 partial
c 137	15	1.1	2219	1	T62436	Human L5/3 partial
c 138	15	1.1	2262	1	Q79729	Full-length human
c 139	15	1.1	2262	1	T62439	Human L5/3 constru
140	15	1.1	2325	1	T04156	Enzyme Q36 coding
c 141	15	1.1	2352	1	V20575	Human pro-tumour n
c 142	15	1.1	2352	1	V73948	Human TNF-alpha co
c 143	15	1.1	2355	1	V80664	Human DNAX toll-li
144	15	1.1	2376	1	V72590	Mouse neurotrypsin
145	15	1.1	2471	1	T58548	Bacillus lichenifo
146	15	1.1	2614	1	X19027	Mouse serine prote
c 147	15	1.1	2640	1	V22790	Clas I S-receptor
c 148	15	1.1	2717	1	T02504	Pectin-lyase-I gen
c 149	15	1.1	2749	1	Q63492	S-Locus receptor (
c 150	15	1.1	2780	1	V32925	Brassica sp. S-rec
151	15	1.1	2880	1	X19729	Rat VR1 capsaicin
152	15	1.1	3073	1	T04158	Enzyme Q36 coding
153	15	1.1	3098	1	Q36363	Defective tyrosine
154	15	1.1	3098	1	Q70808	Protein kinase (HR
155	15	1.1	3098	1	Q92943	Saccharomyces cere
156	15	1.1	3125	1	N70455	5'-3' sequence of
c 157	15	1.1	3150	1	V74654	Staphylococcus aur
158	15	1.1	3305	1	Q39967	PKC-alpha cDNA. Ne
159	15	1.1	3372	1	N80755	Encodes all HAV st
c 160	15	1.1	3384	1	T86165	Nucleotide sequenc
161	15	1.1	3627	1	V08574	CSB2 coding sequen
162	15	1.1	3684	1	V15222	Bacillus thuringie
c 163	15	1.1	3809	1	T61382	Parathyroid calciu
c 164	15	1.1	3809	1	T95859	Human parathyroid
c 165	15	1.1	3809	1	V26964	Human parathyroid
c 166	15	1.1	3809	1	V82485	Human parathyroid
c 167	15	1.1	3921	1	T31300	Rice Xa21 disease
c 168	15	1.1	4086	1	Q51033	Human myoD gene an
c 169	15	1.1	4131	1	T89290	Dogfish shark kidn
c 170	15	1.1	4131	1	T95860	Rat kidney cell ca
c 171	15	1.1	4131	1	V26965	Rat kidney calcium
c 172	15	1.1	4131	1	V82486	Rat parathyroid ca
173	15	1.1	4185	1	V52306	Streptococcus pneu
174	15	1.1	4219	1	V74523	Staphylococcus aur
175	15	1.1	4359	1	V40711	Aldehyde oxidase g
176	15	1.1	4412	1	V40710	Aldehyde oxidase g
177	15	1.1	4440	1	T68322	Human multidrug re
178	15	1.1	4602	1	V59574	Human secreted pro
c 179	15	1.1	4879	1	V74400	Staphylococcus aur
c 180	15	1.1	5006	1	T61381	Parathyroid calciu
c 181	15	1.1	5006	1	T95858	Human parathyroid
c 182	15	1.1	5006	1	V26963	Human parathyroid
c 183	15	1.1	5006	1	V82484	Human parathyroid
c 184	15	1.1	5125	1	Q29703	IRS-1. Purified nu
185	15	1.1	5169	1	T06001	Streptomyces wedmo
186	15	1.1	5238	1	V55846	GTPase activating
c 187	15	1.1	5275	1	T95857	Bovine parathyroid
c 188	15	1.1	5275	1	V26962	Bovine parathyroid
c 189	15	1.1	5275	1	V82483	Bovine parathyroid
c 190	15	1.1	5309	1	Q10280	Complete sequence
191	15	1.1	5448	1	V65229	DNA encoding a S.
c 192	15	1.1	6256	1	T31299	Rice Xa21 disease
193	15	1.1	6399	1	X13013	Enterococcus faeca
c 194	15	1.1	6469	1	Q11690	Entire sequence of
195	15	1.1	6948	1	X12941	Enterococcus faeca
c 196	15	1.1	7204	1	X23527	O. longistaminta X
c 197	15	1.1	7451	1	V05856	Complete sequence
c 198	15	1.1	7571	1	V52135	Streptococcus pneu
c 199	15	1.1	7664	1	X13312	Enterococcus faeca
c 200	15	1.1	8051	1	T72685	Sugar biosynthesis
c 201	15	1.1	8160	1	X25774	S.erythraea erythr
c 202	15	1.1	8169	1	V26609	Actinomadura hibis
203	15	1.1	9271	1	V23080	Fragment HGJ2141 o
204	15	1.1	9395	1	T76930	GT110 gene cDNA se
205	15	1.1	9408	1	V68396	Human BAZ2-alpha c
206	15	1.1	9493	1	T00129	Hepatitis GB virus
207	15	1.1	9493	1	T59784	Hepatitis GB virus
208	15	1.1	10708	1	V69286	Sequence of mouse
209	15	1.1	10820	1	X20527	Polynucleotide seq
210	15	1.1	10974	1	V52347	Streptococcus pneu
211	15	1.1	12036	1	Q04668	FHA structural gen
212	15	1.1	12665	1	V52267	Streptococcus pneu
213	15	1.1	13154	1	X13275	Enterococcus faeca
c 214	15	1.1	13340	1	X23522	O. longistaminata
c 215	15	1.1	13811	1	X20649	Polynucleotide seq
216	15	1.1	14051	1	V74414	Staphylococcus aur
c 217	15	1.1	17378	1	X20510	Polynucleotide seq
218	15	1.1	17612	1	V23494	Pseudomonas Xpc, O
c 219	15	1.1	19142	1	X20580	Polynucleotide seq
220	15	1.1	19446	1	V52184	Streptococcus pneu
c 221	15	1.1	19639	1	X23524	O. longistaminata
c 222	15	1.1	22191	1	X20600	Polynucleotide seq
223	15	1.1	31517	1	X13117	Enterococcus faeca
224	15	1.1	49272	1	V35000	Mycobacteriophage
c 225	15	1.1	53526	1	T94101	Human PKD1 gene. H
c 226	15	1.1	53577	1	T18551	Human polycystic k
c 227	15	1.1	53577	1	T94108	Human PKD1 locus b
c 228	15	1.1	110000	1	V30458_1	Continuation (2 of
229	15	1.1	110000	1	V21209_00	Methanococcus jann
230	15	1.1	110000	1	V21209_03	Continuation (4 of
231	15	1.1	110000	1	V21209_12	Continuation (13 o
c 232	15	1.1	110000	1	V21209_14	Continuation (15 o
c 233	15	1.1	110000	1	V30459_1	Continuation (2 of
234	15	1.1	134525	1	Q04525	Total base sequenc
c 235	14	1.0	20	1	Q28443	HIV-1 ribozyme #1.
c 236	14	1.0	21	1	T01664	Peptide nucleic ac
c 237	14	1.0	21	1	T11998	CMV antisense olig
c 238	14	1.0	21	1	X17915	Anti-CMV oligonucl
c 239	14	1.0	24	1	Q30207	HCV-US anti-sense
c 240	14	1.0	27	1	V98185	Human EGF-R hammer
c 241	14	1.0	29	1	V93242	Human B-raf hammer
c 242	14	1.0	32	1	V00369	Bacillus thuringie
c 243	14	1.0	36	1	T54406	Human IL-5 hammerh
c 244	14	1.0	40	1	Q88332	Maize alpha-tubuli
245	14	1.0	46	1	X22921	DE19736591 primer
c 246	14	1.0	46	1	X22925	DE19736591 primer
247	14	1.0	54	1	Q48756	TDH (52-78) primer
248	14	1.0	125	1	X12672	Human biallelic po
c 249	14	1.0	129	1	X10430	Human biallelic po
c 250	14	1.0	141	1	V76149	Staphylococcus aur
251	14	1.0	153	1	V75664	Staphylococcus aur
c 252	14	1.0	159	1	Q65715	CMP-NeuAc hydroxyl

c	253	14	1.0	159	1	T40843	Serine protease nf
	254	14	1.0	166	1	T22272	Human gene signatu
	255	14	1.0	177	1	T43883	Mutated human immu
	256	14	1.0	177	1	T27788	Mutated human immu
c	257	14	1.0	195	1	T67548	H. pylori secreted
	258	14	1.0	198	1	V24785	H. pylori ORF 06ep
	259	14	1.0	200	1	X39511	Human secreted pro
c	260	14	1.0	215	1	V76480	Staphylococcus aur
c	261	14	1.0	219	1	Q43595	Synthetic PTHLP ge
	262	14	1.0	240	1	Q11971	AaIT scorpion toxi
	263	14	1.0	252	1	T67640	H. pylori secreted
c	264	14	1.0	259	1	T23925	Human gene signatu
c	265	14	1.0	271	1	Q04648	Modified kringle d
c	266	14	1.0	271	1	V75308	Staphylococcus aur
c	267	14	1.0	274	1	T25165	Human gene signatu
c	268	14	1.0	297	1	T25681	Human gene signatu
c	269	14	1.0	303	1	V89591	EST clone CN951. N
	270	14	1.0	315	1	Q84029	pMON5974 encodes (
	271	14	1.0	317	1	V90674	Nucleotide sequenc
	272	14	1.0	321	1	Q59801	Human brain Expres
	273	14	1.0	321	1	V90720	Nucleotide sequenc
	274	14	1.0	323	1	T27924	PRLTS gene exon 2
	275	14	1.0	323	1	T27167	PRLTS coding seque
	276	14	1.0	330	1	Q84025	pMON5968 encodes (
c	277	14	1.0	331	1	V87021	EST clone BG142. N
	278	14	1.0	332	1	Q68095	Sequence encoding
	279	14	1.0	333	1	Q68092	Sequence encoding
	280	14	1.0	333	1	Q68102	Sequence encoding
	281	14	1.0	333	1	Q68096	Sequence encoding
	282	14	1.0	333	1	Q68104	Sequence encoding
	283	14	1.0	333	1	Q68097	Sequence encoding
	284	14	1.0	333	1	Q68103	Sequence encoding
	285	14	1.0	333	1	Q68093	Sequence encoding
	286	14	1.0	333	1	Q68098	Sequence encoding
	287	14	1.0	333	1	Q68099	Sequence encoding
	288	14	1.0	336	1	Q84007	pMON5901 encodes (
	289	14	1.0	336	1	Q84009	pMON5901 encodes (
	290	14	1.0	336	1	Q84010	pMON5969 encodes (
	291	14	1.0	336	1	Q84011	pMON5976 encodes (
	292	14	1.0	336	1	Q84012	pMON5941 encodes (
	293	14	1.0	336	1	Q84013	pMON5976 encodes (
	294	14	1.0	336	1	Q84014	pMON5941 encodes (
	295	14	1.0	336	1	Q84021	pMON5960 encodes (
	296	14	1.0	336	1	Q84022	pMON5961 encodes (
	297	14	1.0	336	1	Q84023	pMON5962 encodes (
	298	14	1.0	336	1	Q84024	pMON5963 encodes (
	299	14	1.0	336	1	Q84026	pMON5970 encodes (
	300	14	1.0	336	1	Q84027	pMON5972 encodes (
	301	14	1.0	336	1	Q84028	pMON5973 encodes (
	302	14	1.0	336	1	Q84030	pMON5975 encodes (
	303	14	1.0	336	1	Q84031	pMON5977 encodes (
	304	14	1.0	339	1	Q68081	Sequence of plasmi
	305	14	1.0	339	1	Q68082	Sequence of plasmi
	306	14	1.0	339	1	Q68185	Sequence encoding
	307	14	1.0	339	1	Q68184	Sequence encoding
	308	14	1.0	339	1	Q68110	Sequence encoding
	309	14	1.0	339	1	Q68108	Sequence encoding
	310	14	1.0	339	1	Q68109	Sequence encoding
	311	14	1.0	339	1	Q84015	pMON5978 encodes (
	312	14	1.0	339	1	Q84016	pMON5978 encodes (
	313	14	1.0	339	1	Q84017	pMON5967 encodes (
	314	14	1.0	339	1	Q84032	pMON5980 encodes (
	315	14	1.0	340	1	Q68186	Sequence encoding
	316	14	1.0	342	1	Q84020	pMON5979 encodes (
	317	14	1.0	345	1	Q61337	Human brain Expres
c	318	14	1.0	359	1	T75248	Nucleotide sequenc
	319	14	1.0	360	1	Q84004	pMON5853 encodes (
	320	14	1.0	360	1	Q84006	pMON5872 encodes (
	321	14	1.0	361	1	T26578	Human gene signatu
	322	14	1.0	362	1	V20261	Probe (162) for mi
	323	14	1.0	378	1	Q84008	pMON5887 encodes (
c	324	14	1.0	381	1	T33511	Infectious laryngo
	325	14	1.0	384	1	V86069	EST clone D14. New
	326	14	1.0	391	1	V89105	EST clone BX141. N
	327	14	1.0	396	1	N90326	Hepatitis C virus
	328	14	1.0	396	1	N92096	Sequence of the he
c	329	14	1.0	400	1	X40927	Human secreted pro
	330	14	1.0	402	1	V70394	Nucleic acid seque
	331	14	1.0	408	1	Q68187	Sequence encoding
	332	14	1.0	408	1	Q84033	pMON5853 encodes (
	333	14	1.0	408	1	Q95148	Human interleukin-
	334	14	1.0	409	1	V86576	EST clone AW106. N
	335	14	1.0	414	1	Q68188	Sequence encoding
c	336	14	1.0	414	1	Q84005	pMON5853 encodes (
	337	14	1.0	419	1	T30730	Mouse cryptdin 5 g
c	338	14	1.0	419	1	T47254	(DSM 10104) human
c	339	14	1.0	420	1	X24811	Hypersensitive res
	340	14	1.0	421	1	T30743	Mouse cryptdin 5 c
	341	14	1.0	422	1	T26471	Human gene signatu
	342	14	1.0	429	1	T68026	H. pylori secreted
c	343	14	1.0	430	1	V90253	EST clone D1516. N
	344	14	1.0	443	1	Q05206	Primer binding to
	345	14	1.0	461	1	X34704	DNA sequence of mo
	346	14	1.0	479	1	Q37619	Vdelta2 (cell line
c	347	14	1.0	485	1	V34604	Mycobacterium vacc
c	348	14	1.0	485	1	V34570	M. vaccae antigen
	349	14	1.0	486	1	T70120	Clone C-11-3 from
	350	14	1.0	511	1	V69351	Rice glycogenin cl
	351	14	1.0	515	1	X21179	Polynucleotide seq
c	352	14	1.0	523	1	Q56098	Probe for Cryptosp
	353	14	1.0	526	1	V84494	Human secreted pro
c	354	14	1.0	536	1	X13610	Enterococcus faeca
c	355	14	1.0	540	1	N70767	Sequence of the na
	356	14	1.0	556	1	Q37621	Vdelta3 (cell line
	357	14	1.0	556	1	Q37618	Vdelta2 (cell line
c	358	14	1.0	568	1	Q84670	Yeast presequence
c	359	14	1.0	568	1	Q70273	Yeast presequence
c	360	14	1.0	576	1	T67669	H. pylori cell env
c	361	14	1.0	583	1	T60819	Guanylate cyclase
c	362	14	1.0	583	1	T65115	Human GCAP-II prec
	363	14	1.0	602	1	T58577	Cryptosporidium pa
	364	14	1.0	624	1	N71272	Sequence of adult
c	365	14	1.0	644	1	N60396	Sequence of promot
	366	14	1.0	647	1	Q73017	Hepatitis Type-C v
	367	14	1.0	648	1	Q67257	Silver fox growth
c	368	14	1.0	648	1	X54627	Human IL-3 recepto
	369	14	1.0	657	1	T47185	HTLV-I gp24 gag ge
c	370	14	1.0	675	1	V26689	Human novel secret
	371	14	1.0	687	1	T41495	DNA encoding MAGE-
c	372	14	1.0	695	1	V53471	DNA encoding a Sta
	373	14	1.0	705	1	T38006	Clone MSRV2sPR iso
c	374	14	1.0	711	1	X34231	Mycobacterium spec
	375	14	1.0	712	1	V27391	Streptococcus pneu
c	376	14	1.0	714	1	V75009	Staphylococcus aur
	377	14	1.0	717	1	X22939	Chlamydomonas sp.
c	378	14	1.0	721	1	V84605	Human secreted pro
	379	14	1.0	723	1	T86281	Soybean albumin 1
	380	14	1.0	723	1	V65275	DNA encoding a S.
c	381	14	1.0	738	1	N70037	Insulin-like growt
	382	14	1.0	748	1	T02826	Multiple sclerosis
	383	14	1.0	748	1	T38004	Clone MSRV-2EL1. D
	384	14	1.0	748	1	V43126	Multiple sclerosis
	385	14	1.0	753	1	T67487	H. pylori surface
c	386	14	1.0	759	1	V04597	Flea serine protea
	387	14	1.0	762	1	T73988	Sequence 40 from W
	388	14	1.0	762	1	V23289	Synthetic green fl
	389	14	1.0	772	1	X20015	Enterococcus faeca
	390	14	1.0	774	1	Q92407	Human cyclin A pro
	391	14	1.0	780	1	Q67206	Canine growth horm
	392	14	1.0	780	1	Q67207	Gly184, Ala186-Can
	393	14	1.0	783	1	Q66887	Human lymphocyte c
	394	14	1.0	798	1	T88156	E. coli Tsh autotr
	395	14	1.0	798	1	X16086	DNA encoding wild-
c	396	14	1.0	800	1	X13673	Enterococcus faeca
	397	14	1.0	801	1	T68280	H. pylori putative
	398	14	1.0	805	1	X18954	Fructose:glucose r

c 399	14	1.0	807	1	Q98735	Barley Ltp2 gene p
c 400	14	1.0	828	1	T68075	H. pylori secreted
c 401	14	1.0	839	1	V34717	Human Fanconi I cD
402	14	1.0	840	1	X20014	Enterococcus faeca
403	14	1.0	845	1	T66947	Chicken interleuki
c 404	14	1.0	850	1	T40855	Serine protease nf
405	14	1.0	857	1	V75197	Staphylococcus aur
c 406	14	1.0	858	1	V45175	Human LEA-motif de
407	14	1.0	861	1	V43021	Streptococcus pneu
c 408	14	1.0	867	1	T74471	Open reading frame
c 409	14	1.0	879	1	T01341	Human FK506 bindin
c 410	14	1.0	894	1	N70391	Human recombinant
c 411	14	1.0	894	1	N70036	Insulin-like growt
c 412	14	1.0	897	1	V24697	H. pylori ORF 14ae
c 413	14	1.0	912	1	V46315	Human secreted pro
c 414	14	1.0	913	1	Q70048	Dirofilaria immiti
415	14	1.0	925	1	T15611	CROC-4 cDNA encode
416	14	1.0	925	1	V16740	cDNA encoding huma
417	14	1.0	940	1	X21054	Polynucleotide seq
c 418	14	1.0	945	1	V90853	Nucleotide sequenc
419	14	1.0	945	1	X25733	B.subtilis cystein
420	14	1.0	950	1	Q11972	Scorpion toxin exp
c 421	14	1.0	954	1	X20092	Enterococcus faeca
422	14	1.0	963	1	V55148	Multi-functional h
423	14	1.0	963	1	V55150	Multi-functional h
c 424	14	1.0	971	1	X37469	Human secreted pro
c 425	14	1.0	972	1	T34189	PcpD coding sequen
426	14	1.0	972	1	V55149	Multi-functional h
427	14	1.0	972	1	V55151	Multi-functional h
428	14	1.0	981	1	V12756	A. faecalis JM3 ni
c 429	14	1.0	981	1	X16591	Helicobacter pylor
430	14	1.0	1001	1	X20478	Human secreted pro
c 431	14	1.0	1004	1	X13479	Enterococcus faeca
432	14	1.0	1017	1	V24931	H. pylori cell env
c 433	14	1.0	1023	1	X13585	Enterococcus faeca
c 434	14	1.0	1023	1	X34232	Mycobacterium spec
c 435	14	1.0	1025	1	V18441	Unknown DNA sequen
c 436	14	1.0	1034	1	X14407	H. pylori GHPO 604
437	14	1.0	1068	1	X13571	Enterococcus faeca
c 438	14	1.0	1083	1	T14024	Drosophila dCREB2-
439	14	1.0	1095	1	V99747	IL-1 alpha propiec
c 440	14	1.0	1097	1	V44860	Clone BG142_1 codi
441	14	1.0	1101	1	V25033	H. pylori cell env
442	14	1.0	1101	1	V25034	H. pylori cell env
c 443	14	1.0	1103	1	V05139	cDNA encoding muri
444	14	1.0	1110	1	V24662	H. pylori ORF 05gp
445	14	1.0	1115	1	V48115	Nucleotide sequenc
446	14	1.0	1116	1	V25108	H. pylori ORF 06ap
c 447	14	1.0	1125	1	N91423	Sequence of heat-r
448	14	1.0	1125	1	Q70705	Plasmin receptor D
c 449	14	1.0	1125	1	T67935	H. pylori cytoplas
450	14	1.0	1127	1	V12757	A. faecalis JM3 ni
c 451	14	1.0	1138	1	V46314	Human secreted pro
452	14	1.0	1140	1	V71081	Alpha-actinin acti
453	14	1.0	1143	1	T34428	Eucalyptus AGE1 cD
454	14	1.0	1187	1	V74711	Staphylococcus aur
c 455	14	1.0	1200	1	Q05728	Gene encoding glut
456	14	1.0	1200	1	V24539	Full length mouse
457	14	1.0	1200	1	V74138	Mouse FLAME-2 cDNA
c 458	14	1.0	1204	1	X14194	H. pylori GHPO 885
459	14	1.0	1204	1	X14013	H. pylori GHPO 169
c 460	14	1.0	1221	1	X30447	H. pylori outer me
461	14	1.0	1224	1	T15958	Canine cholecystok
c 462	14	1.0	1224	1	T67867	H. pylori cell env
c 463	14	1.0	1236	1	Q58033	TRP-1 promoter. DN
464	14	1.0	1238	1	Q70537	Nicotineamide aden
c 465	14	1.0	1239	1	T68012	H. pylori secreted
c 466	14	1.0	1239	1	X07132	Staphylococcus aur
c 467	14	1.0	1239	1	X07112	Staphylococcus aur
468	14	1.0	1247	1	Q41354	Human GDF-1 coding
469	14	1.0	1247	1	Q38862	Morphogen GDF-1 co
470	14	1.0	1247	1	Q58055	Human morphogenic
471	14	1.0	1247	1	Q67315	Human GDF-1(fx) mo
472	14	1.0	1247	1	Q45120	Human GDF-1(fx) mo
473	14	1.0	1247	1	Q67402	Human GDF-1(fx) mo
474	14	1.0	1247	1	T97883	cDNA sequence enco
475	14	1.0	1247	1	V10351	Human GDF-1 cDNA.
476	14	1.0	1247	1	V19538	Human GDF-1 (fx) p
477	14	1.0	1247	1	V32588	Human GDF-1 cDNA.
478	14	1.0	1254	1	Q10952	Insert from pIG1 e
c 479	14	1.0	1255	1	T13981	Human body weight
c 480	14	1.0	1255	1	V09078	Human C5 gene cDNA
c 481	14	1.0	1266	1	X25773	S.erythraea erythr
c 482	14	1.0	1268	1	Q26713	Encodes exon I of
483	14	1.0	1275	1	V59143	Phaffia rhodozyma
c 484	14	1.0	1280	1	Q51487	cDNA encoding orni
485	14	1.0	1290	1	Q03061	Human T-cell leuke
486	14	1.0	1306	1	V52019	Helicobacter polyp
c 487	14	1.0	1307	1	Q31804	Brassica thioester
c 488	14	1.0	1307	1	Q65407	Brassica campestri
c 489	14	1.0	1307	1	Q92309	Brassica acyl thio
c 490	14	1.0	1307	1	V15236	Brassica campestri
c 491	14	1.0	1314	1	T51410	Human ribosomal pr
492	14	1.0	1315	1	Q22997	Human ZP3 gene. Hu
c 493	14	1.0	1328	1	Q94882	Barley Ltp2 gene.
494	14	1.0	1329	1	V71080	Green fluorescent
495	14	1.0	1333	1	V05317	Mouse haematopoiet
c 496	14	1.0	1335	1	T47875	K. pneumoniae alco
497	14	1.0	1338	1	Q99004	Canine cholecystok
498	14	1.0	1338	1	T10093	Canine cholecystok
499	14	1.0	1338	1	T15959	Canine cholecystok
500	14	1.0	1343	1	T98589	DNA encoding a S.
c 501	14	1.0	1347	1	T41699	Onchocerca volvulu
c 502	14	1.0	1356	1	T42060	Bovine rotavirus V
503	14	1.0	1357	1	T66555	Rabies virus nucle
504	14	1.0	1383	1	V42055	Kurthia sp. biotin
c 505	14	1.0	1386	1	V59647	Human secreted pro
c 506	14	1.0	1389	1	V21235	Homo sapiens clone
507	14	1.0	1399	1	X20017	Enterococcus faeca
508	14	1.0	1416	1	X30587	H. pylori outer me
c 509	14	1.0	1434	1	X16007	DNA encoding an an
c 510	14	1.0	1435	1	X14025	H. pylori GHPO 525
c 511	14	1.0	1437	1	Q36687	Sequence encoding
c 512	14	1.0	1437	1	Q48234	Cytochrome C gene.
c 513	14	1.0	1437	1	T71594	Mycobacterium tube
c 514	14	1.0	1437	1	V29069	Mycobacterium tube
c 515	14	1.0	1437	1	V42598	M. tuberculosis 58
516	14	1.0	1440	1	Q47998	Sequence encoding
517	14	1.0	1440	1	V74943	Staphylococcus aur
518	14	1.0	1448	1	T84017	DNA encoding a sul
519	14	1.0	1448	1	V53413	DNA encoding a sir
520	14	1.0	1450	1	Q99003	Canine cholecystok
521	14	1.0	1450	1	T10092	Canine cholecystok
c 522	14	1.0	1463	1	V00123	Rat hexokinase enc
c 523	14	1.0	1488	1	X03981	Thermus flavus TE3
c 524	14	1.0	1493	1	V01889	Human OTK27 gene.
525	14	1.0	1500	1	X20016	Enterococcus faeca
526	14	1.0	1508	1	T37312	Aromatic acyl tran
527	14	1.0	1509	1	V24861	H. pylori secreted
528	14	1.0	1509	1	V24959	H. pylori secreted
529	14	1.0	1512	1	Q14274	Chimpanzee HCV clo
530	14	1.0	1512	1	Q73003	Hepatitis Type C v
531	14	1.0	1512	1	Q98204	Hepatitis C virus
532	14	1.0	1512	1	V70801	Insert of a HCV cl
533	14	1.0	1512	1	V70547	Insert of a HCV cl
534	14	1.0	1513	1	X14006	H. pylori GHPO 144
535	14	1.0	1514	1	Q22988	Sequence of the SA
536	14	1.0	1517	1	Q25268	Protease inhibitor
c 537	14	1.0	1523	1	Q91523	Soluble murine MPL
c 538	14	1.0	1529	1	Q88328	Maize alpha-tubuli
539	14	1.0	1530	1	N50275	Sequence from pATK
c 540	14	1.0	1539	1	T17153	Mycobacterium tube
c 541	14	1.0	1548	1	Q13868	Insert from clone
c 542	14	1.0	1552	1	T72713	Drosophila inhibit
543	14	1.0	1558	1	Q27988	Protease from S. A
544	14	1.0	1560	1	V72221	Autographa califor

c	545	14	1.0	1576	1	Q10226
	546	14	1.0	1584	1	V84358
	547	14	1.0	1586	1	Q27987
	548	14	1.0	1587	1	X13606
c	549	14	1.0	1592	1	V44638
c	550	14	1.0	1596	1	V82381
	551	14	1.0	1597	1	V43827
c	552	14	1.0	1599	1	V38531
	553	14	1.0	1600	1	Q85770
	554	14	1.0	1602	1	Q72217
	555	14	1.0	1605	1	V72222
c	556	14	1.0	1611	1	V21655
c	557	14	1.0	1612	1	V44595
	558	14	1.0	1620	1	Q00543
c	559	14	1.0	1630	1	N70315
	560	14	1.0	1630	1	X14097
c	561	14	1.0	1631	1	V44636
	562	14	1.0	1633	1	V43824
	563	14	1.0	1635	1	V71073
	564	14	1.0	1635	1	V71074
	565	14	1.0	1667	1	V52050
	566	14	1.0	1689	1	T08083
	567	14	1.0	1721	1	T39752
c	568	14	1.0	1724	1	T40082
	569	14	1.0	1735	1	T77840
	570	14	1.0	1738	1	T98569
	571	14	1.0	1739	1	T74472
	572	14	1.0	1757	1	Q49428
	573	14	1.0	1757	1	T94666
c	574	14	1.0	1758	1	N90600
c	575	14	1.0	1758	1	Q04719
c	576	14	1.0	1758	1	Q06099
c	577	14	1.0	1758	1	Q20201
c	578	14	1.0	1758	1	T75084
c	579	14	1.0	1761	1	T12919
c	580	14	1.0	1761	1	T12920
c	581	14	1.0	1761	1	V07282
c	582	14	1.0	1763	1	T12918
c	583	14	1.0	1765	1	T12921
c	584	14	1.0	1767	1	T12922
c	585	14	1.0	1770	1	Q79692
	586	14	1.0	1770	1	T63432
c	587	14	1.0	1779	1	Q31651
	588	14	1.0	1779	1	T85394
c	589	14	1.0	1782	1	N90128
c	590	14	1.0	1784	1	N40163
c	591	14	1.0	1784	1	N40145
	592	14	1.0	1788	1	Q44979
	593	14	1.0	1788	1	T16059
	594	14	1.0	1788	1	T63431
	595	14	1.0	1788	1	V66968
	596	14	1.0	1788	1	V42805
	597	14	1.0	1799	1	V07920
	598	14	1.0	1812	1	X18925
c	599	14	1.0	1813	1	Q70903
	600	14	1.0	1814	1	N70309
c	601	14	1.0	1814	1	X04373
	602	14	1.0	1815	1	V71031
	603	14	1.0	1818	1	V71023
	604	14	1.0	1821	1	V71034
	605	14	1.0	1824	1	V71025
c	606	14	1.0	1827	1	Q03685
c	607	14	1.0	1827	1	T27599
c	608	14	1.0	1827	1	V20403
c	609	14	1.0	1830	1	Q29765
c	610	14	1.0	1830	1	Q29695
c	611	14	1.0	1830	1	Q98695
c	612	14	1.0	1830	1	T14580
c	613	14	1.0	1830	1	T27598
c	614	14	1.0	1830	1	T27600
c	615	14	1.0	1830	1	T27601
c	616	14	1.0	1832	1	T12924
	617	14	1.0	1836	1	Q22196

Clone pGEM-hRARgam
Streptococcus pneu
Protease from S. A
Enterococcus faeca
Human uncoupling p
Full length human
Atrazine chlorohyd
DNA marker of meta
Low affinity nerve
Human adrenergic r
Baculovirus ISP DN
AAV4 Rep 68 gene.
Human respiration
Vampire bat plasmi
Sequence encoding
H. pylori GHPO 137
Human uncoupling p
Atrazine chlorohyd
CDK2-green fluores
Green fluorescent
Helicobacter polyp
Alpha-1,3/4-fucosi
Macaque mucosal ad
M. tuberculosis RN
Human melanoma ass
DNA encoding a S.
Open reading frame
Cytochrome P450 ho
Petunia flavonoid
cDNA encoding huma
Sequence encoding
DNA encoding human
Human serum albumi
Human serum albumi
Human serum albumi
Human serum albumi
Human semaphorin W
Human serum albumi
Human serum albumi
Human serum albumi
Alcaligenes eutrop
HCV RNA-dependent
Bacillus caldotena
Saccharomyces cere
DNA encoding matur
Sequence of protei
Sequence of protei
Murine Ikaros gene
Murine Ikaros cDNA
Hepatitis C virus
Murine Ikaros enco
Mouse Ikaros isofo
Helicobacter pylor
Phaseolus lunatus
Cold acclimatizati
Sequence of bovine
Human secreted pro
Erk2-green floures
Green flourescent
p38-green flouresc
p38-green flouresc
cDNA sequence enco
HSA gene with fuse
Human serum albumi
HSA gene. Improved
HSA gene. Expressi
Human serum albumi
Cancer metastasis
HSA gene with N-te
HSA gene with fuse
HSA gene with C-te
Gene coding for HS
Gene coding for P6

	618	14	1.0	1839	1	Q29147
c	619	14	1.0	1839	1	Q29147
	620	14	1.0	1842	1	T68244
c	621	14	1.0	1845	1	V25052
c	622	14	1.0	1851	1	Q38249
c	623	14	1.0	1851	1	Q38264
c	624	14	1.0	1851	1	Q38279
	625	14	1.0	1851	1	X27845
c	626	14	1.0	1854	1	Q21691
c	627	14	1.0	1862	1	Q46007
c	628	14	1.0	1863	1	N60399
c	629	14	1.0	1865	1	V41728
	630	14	1.0	1868	1	T59712
c	631	14	1.0	1872	1	Q39220
c	632	14	1.0	1872	1	V21649
c	633	14	1.0	1872	1	V21656
c	634	14	1.0	1873	1	Q01648
c	635	14	1.0	1886	1	Q04453
c	636	14	1.0	1886	1	Q05966
	637	14	1.0	1890	1	Q89781
	638	14	1.0	1893	1	V71033
	639	14	1.0	1896	1	V71022
	640	14	1.0	1902	1	V71118
c	641	14	1.0	1903	1	Q10389
c	642	14	1.0	1903	1	T05196
	643	14	1.0	1905	1	N90395
	644	14	1.0	1906	1	N70306
	645	14	1.0	1906	1	Q92784
	646	14	1.0	1907	1	X20307
	647	14	1.0	1908	1	V71079
c	648	14	1.0	1919	1	Q11055
	649	14	1.0	1926	1	Q79624
	650	14	1.0	1929	1	V58275
	651	14	1.0	1929	1	V58277
	652	14	1.0	1934	1	T45793
	653	14	1.0	1940	1	V53551
c	654	14	1.0	1940	1	V41732
	655	14	1.0	1942	1	Q37616
	656	14	1.0	1958	1	V58276
c	657	14	1.0	1959	1	T85095
	658	14	1.0	1970	1	V28138
	659	14	1.0	1971	1	V58278
	660	14	1.0	1978	1	Q72212
c	661	14	1.0	1983	1	V24954
c	662	14	1.0	1983	1	V24985
c	663	14	1.0	1986	1	T48588
c	664	14	1.0	1986	1	T78596
	665	14	1.0	1987	1	T11624
	666	14	1.0	1988	1	V80364
	667	14	1.0	1997	1	T11600
	668	14	1.0	1998	1	Q72213
	669	14	1.0	2000	1	T77839
c	670	14	1.0	2003	1	V84571
	671	14	1.0	2004	1	T11599
	672	14	1.0	2004	1	V25065
	673	14	1.0	2005	1	Q72211
c	674	14	1.0	2007	1	Q27287
	675	14	1.0	2007	1	V25147
c	676	14	1.0	2015	1	N60107
	677	14	1.0	2016	1	Q02887
c	678	14	1.0	2019	1	Q85643
	679	14	1.0	2028	1	Q48760
	680	14	1.0	2038	1	V33060
	681	14	1.0	2049	1	T16062
	682	14	1.0	2049	1	V66971
	683	14	1.0	2049	1	V42808
c	684	14	1.0	2055	1	N30110
	685	14	1.0	2055	1	X34159
	686	14	1.0	2057	1	T45098
	687	14	1.0	2061	1	X34160
c	688	14	1.0	2064	1	N92583
c	689	14	1.0	2064	1	T66701
	690	14	1.0	2082	1	V74522

DNA encoding p34 f
DNA encoding p34 f
H. pylori inner me
H. pylori cell env
HCV CKS-ENV recomb
HCV CKS-ENV recomb
HCV CKS-ENV recomb
Mutant lipase codi
pHCV-104 - recombi
cDNA encoding chim
Sequence of the pr
DNA encoding the m
Endotoxin CryIa(c)
Carrot reverse tra
AAV4 Rep gene. Ade
AAV4 Rep 78 gene.
BUF-3 gene for hum
Arp 4 gene. New St
Sequence encoding
Human alpha 1c adr
Jnk1-green floures
Erk1-green floures
Jnk1-green floures
Encodes human Reti
Human retinoic aci
Genomic/cDNA compo
Sequence encoding
Mullerian inhibiti
Borrelia burgdorfe
Green fluorescent
Clone 19 encoding
DNA encoding malol
Fluorescent calmod
Fluorescent calmod
Heliothis ecdysone
DNA encoding a for
Codon-optimised RA
TCR delta protein
Fluorescent calmod
Human transforming
Human HFGAN72 rece
Fluorescent calmod
Truncated human al
H. pylori inner me
H. pylori ORF 06ep
cDNA coding for CM
Cytidine monophosp
Human truncated al
Human homeobox gen
Human alpha-1C adr
Human alpha-1C adr
Human melanoma ass
Human secreted pro
Human alpha-1C adr
H. pylori cell env
Human alpha-1C adr
DNA encoding TAP.
H. pylori cell env
Sequence encoding
cDNA of human plac
Poly-beta-hydroxya
GAT-2 GABA transpo
Oryza sativa RNA p
Murine Ikaros cDNA
Mouse Ikaros encod
Mouse Ikaros isofo
Sequence encoding
Mycobacterium spec
Cytomegalovirus po
Mycobacterium spec
Sequence of human
Human serum albumi
Staphylococcus aur

691	14	1.0	2085	1	Q81504	OPDE 45 kDa subuni
692	14	1.0	2089	1	T31378	Human alpha-1C3 ad
c 693	14	1.0	2093	1	Q70541	Hepatitis C virus
694	14	1.0	2098	1	X02558	Human B1 cDNA. New
c 695	14	1.0	2127	1	V23246	Human adenylylcycl
c 696	14	1.0	2133	1	N91042	Promoter-enhancer
697	14	1.0	2137	1	Q05675	v-PA_beta. New fib
698	14	1.0	2157	1	V71039	Erk2-green floures
699	14	1.0	2160	1	V71027	Smad2-green floure
700	14	1.0	2165	1	T14054	Fungal signal reco
c 701	14	1.0	2169	1	X23320	N. meningitidis st
702	14	1.0	2172	1	Q56930	Bacillus thuringie
c 703	14	1.0	2175	1	Q29268	Human calcium chan
704	14	1.0	2181	1	V71037	PKB-green flouresc
705	14	1.0	2184	1	V71086	Green fluorescent
706	14	1.0	2192	1	T77838	Human melanoma ass
c 707	14	1.0	2196	1	Q74211	CMVintA promoter a
c 708	14	1.0	2196	1	T01112	CMVintA-GBH termin
c 709	14	1.0	2199	1	T80052	Rice actin 1 gene
710	14	1.0	2206	1	Q70754	Beta tubulin gene
c 711	14	1.0	2214	1	Q70731	TATA-binding prote
712	14	1.0	2217	1	Q66982	Human betaine-GABA
713	14	1.0	2217	1	T16542	Human betaine/GABA
c 714	14	1.0	2220	1	T11022	Urochloa panicoide
715	14	1.0	2247	1	V24920	H. pylori ORF 05ae
716	14	1.0	2247	1	V25134	H. pylori inner me
c 717	14	1.0	2251	1	N30050	Sequence encoding
c 718	14	1.0	2251	1	X40195	Human albumin gene
719	14	1.0	2255	1	T11240	Neisseria meningit
720	14	1.0	2257	1	Q05674	v-PA_alpha2. New f
c 721	14	1.0	2258	1	N60078	Recombinant human
c 722	14	1.0	2262	1	X23322	N. meningitidis st
c 723	14	1.0	2265	1	T14530	HSA:Fc gamma RII g
724	14	1.0	2270	1	N91184	SprB gene encoding
c 725	14	1.0	2274	1	V90770	Nucleotide sequenc
c 726	14	1.0	2280	1	N60395	Sequence constitut
727	14	1.0	2290	1	Q89780	Human alpha 1c adr
c 728	14	1.0	2292	1	V84357	Streptococcus pneu
729	14	1.0	2297	1	V58945	B. breve essential
730	14	1.0	2306	1	T31377	Human alpha-1C2 ad
c 731	14	1.0	2315	1	V07281	Human semaphorin W
c 732	14	1.0	2330	1	Q20759	Alkaline protease
733	14	1.0	2337	1	T94212	Thermotoga maritim
734	14	1.0	2338	1	Q13575	DHR3 gene. DNA enc
735	14	1.0	2341	1	V62155	HSV-2 strain SB5 C
736	14	1.0	2343	1	V36302	Murine guanine nuc
737	14	1.0	2360	1	Q02888	Human placenta-der
c 738	14	1.0	2360	1	Q24438	EGF/HB-EHM. Hepari
739	14	1.0	2364	1	Q12632	CD4-specific CDR-g
c 740	14	1.0	2373	1	Q45455	Sequence encoding
c 741	14	1.0	2379	1	Q10548	Prepro-HSA-V1V2 fu
c 742	14	1.0	2382	1	Q45987	Prepro-HSA-G-CSF c
743	14	1.0	2384	1	Q46543	Drosophila SSRP co
744	14	1.0	2384	1	V09624	D. melanogaster SS
c 745	14	1.0	2387	1	Q48438	Brh-I cDNA. Polype
c 746	14	1.0	2387	1	T45675	Wasp Brh-1 toxin g
747	14	1.0	2394	1	V71088	NFkappaB p65 subun
748	14	1.0	2394	1	V71087	PKB-green fluoresc
749	14	1.0	2395	1	V90864	Nucleotide sequenc
750	14	1.0	2397	1	V71040	Smad4-green floure
751	14	1.0	2418	1	T15598	Laccase-LCC1 gene.
752	14	1.0	2421	1	V71028	Green flourescent
753	14	1.0	2427	1	V07915	Helicobacter pylor
c 754	14	1.0	2430	1	Q04305	Coding region of m
c 755	14	1.0	2430	1	T61550	Murine interleukin
c 756	14	1.0	2430	1	V17655	Mouse interleukin-
c 757	14	1.0	2430	1	V38332	Mouse interleukin-
c 758	14	1.0	2430	1	V08858	Mouse interleukin-
c 759	14	1.0	2430	1	X22407	Murine IL-4 recept
c 760	14	1.0	2433	1	T29396	Apoptosis particip
c 761	14	1.0	2438	1	V38687	Mus musculus SOCS1
762	14	1.0	2454	1	T32864	Tomato P119 gene p
c 763	14	1.0	2455	1	Q45988	G-CSF-(Gly)4-HSA c
c 764	14	1.0	2462	1	X20299	Borrelia burgdorfe
765	14	1.0	2464	1	T45794	Heliothis ecdysone
c 766	14	1.0	2472	1	V74953	Staphylococcus aur
c 767	14	1.0	2503	1	T96475	MSRV-1 clone LTRGA
c 768	14	1.0	2503	1	V43169	Clone LTRGAG12 DNA
c 769	14	1.0	2506	1	T34184	Pentachlorophenol
770	14	1.0	2510	1	Q20690	hGDF-1 and hUOG-1
771	14	1.0	2511	1	V71032	Grk5-green floures
c 772	14	1.0	2516	1	Q49737	Pcp B gene. Novel
773	14	1.0	2529	1	V71024	Grk5-green floures
774	14	1.0	2532	1	V71075	Green fluorescent
775	14	1.0	2537	1	N70917	Sequence encoding
776	14	1.0	2550	1	T47532	Cytomegalovirus To
777	14	1.0	2550	1	T47534	Cytomegalovirus To
778	14	1.0	2562	1	V71076	Protein tyrosine p
779	14	1.0	2575	1	T98572	DNA encoding a S.
780	14	1.0	2582	1	T90543	Maize male fertili
c 781	14	1.0	2591	1	Q45961	HSA-vWF(470-713) f
782	14	1.0	2598	1	V71072	Zap70-green fluore
c 783	14	1.0	2603	1	T72148	DNA encoding trans
784	14	1.0	2616	1	Q37966	Sequence encoding
785	14	1.0	2616	1	V71071	Green fluorescent
786	14	1.0	2623	1	T51715	cDNA for adenoviru
c 787	14	1.0	2629	1	N81338	Protein A gene wit
c 788	14	1.0	2629	1	Q24523	Vasoactive intesti
c 789	14	1.0	2631	1	T75434	Bacillus caldotena
c 790	14	1.0	2631	1	T75432	DNA encoding Bacil
c 791	14	1.0	2631	1	T75433	DNA encoding Bacil
792	14	1.0	2639	1	Q41259	2,2-dialkylglycine
793	14	1.0	2639	1	Q72718	Dialkylglycine dec
c 794	14	1.0	2655	1	V32919	Solanum tuberosum
795	14	1.0	2659	1	Q51608	Moraxella bovis mb
796	14	1.0	2662	1	V53136	Helicobacter leucy
c 797	14	1.0	2666	1	Q98236	Partial rice pyruv
798	14	1.0	2684	1	Q75136	Lactococcus lactis
799	14	1.0	2692	1	Q51114	Sequence encoding
c 800	14	1.0	2694	1	V62145	HSV-2 strain SB5 C
801	14	1.0	2716	1	T42064	Human brain Na+ de
802	14	1.0	2716	1	V33503	Human sodium-lithi
803	14	1.0	2724	1	Q78166	Human cytomegalovi
804	14	1.0	2724	1	T47527	Human cytomegalovi
805	14	1.0	2724	1	T91280	Human cytomegalovi
806	14	1.0	2741	1	V36300	Murine guanine nuc
c 807	14	1.0	2745	1	Q92656	Virulence determin
c 808	14	1.0	2745	1	Q92657	Virulence determin
809	14	1.0	2745	1	T45795	Heliothis ecdysone
c 810	14	1.0	2745	1	V38109	Mycobacterium bovi
c 811	14	1.0	2745	1	V38108	Mycobacterium bovi
c 812	14	1.0	2746	1	V72893	Rabbit protein-cou
c 813	14	1.0	2751	1	X30434	H. pylori cellular
c 814	14	1.0	2760	1	X25097	Bacillus subtilis
c 815	14	1.0	2768	1	Q10502	Polyhydroxybutyrat
c 816	14	1.0	2770	1	T78599	AS-30D tumour Type
c 817	14	1.0	2778	1	V25138	H. pylori cell env
c 818	14	1.0	2784	1	T68270	H. pylori cytoplas
819	14	1.0	2799	1	V71085	PKG-green fluoresc
820	14	1.0	2802	1	V71084	Green fluorescent
c 821	14	1.0	2833	1	Q32648	S receptor kinase
822	14	1.0	2833	1	V36301	Murine guanine nuc
823	14	1.0	2845	1	T93093	Human GCF1 cDNA. P
824	14	1.0	2854	1	V32591	Schwannomin-bindin
c 825	14	1.0	2871	1	Q14807	B.thuringiensis to
c 826	14	1.0	2898	1	T68848	Photorhabdus lumin
827	14	1.0	2899	1	Q86757	Construct comprisi
828	14	1.0	2899	1	T14053	Fungal signal reco
829	14	1.0	2907	1	V71026	p85alpha-green flo
c 830	14	1.0	2911	1	V00133	Hexokinase-glucoki
c 831	14	1.0	2911	1	V00099	Hexokinase-glucoki
c 832	14	1.0	2911	1	V00124	Hexokinase-glucoki
c 833	14	1.0	2911	1	V00098	Hexokinase-glucoki
834	14	1.0	2911	1	V05709	Human Th2/B19 cDNA
835	14	1.0	2913	1	V71035	p85alpha-green flo
836	14	1.0	2917	1	Q86758	Construct comprisi

c	837	14	1.0	2955	1	V20404 Plasmid R-H-R/SK #
	838	14	1.0	2959	1	Q86756 Construct comprisi
	839	14	1.0	2962	1	X21408 targetting region
	840	14	1.0	2965	1	X39658 Renal cancer assoc
c	841	14	1.0	2971	1	N81166 fdhF gene New reco
	842	14	1.0	2991	1	V71078 IkappaB kinase alp
c	843	14	1.0	2991	1	X20288 Borrelia burgdorfe
c	844	14	1.0	2994	1	V29925 tccA gene from the
	845	14	1.0	2994	1	V71077 Green fluorescent
	846	14	1.0	3000	1	Q14319 Pertactin antigen
	847	14	1.0	3000	1	Q14320 Pertactin antigen
	848	14	1.0	3000	1	Q26509 Bordetella paraper
	849	14	1.0	3000	1	Q34566 prn gene. DNA enco
c	850	14	1.0	3012	1	V52012 Helicobacter polyp
	851	14	1.0	3029	1	X20286 Borrelia burgdorfe
	852	14	1.0	3032	1	V20992 Alcaligenes specie
	853	14	1.0	3101	1	X14217 H. pylori GHPO 111
	854	14	1.0	3106	1	T99905 Enterohaemorrhagic
	855	14	1.0	3106	1	V02323 Enterohaemorrhagic
	856	14	1.0	3107	1	V68092 cDNA encoding the
c	857	14	1.0	3110	1	T84234 DNA encoding an au
c	858	14	1.0	3110	1	V53557 DNA encoding 2 Sta
	859	14	1.0	3120	1	V71029 Green flourescent
c	860	14	1.0	3125	1	Q73686 HIV virus-1(LAI) g
	861	14	1.0	3131	1	Q66687 EHEC eae gene asso
	862	14	1.0	3131	1	T99904 Enterohaemorrhagic
	863	14	1.0	3131	1	V02322 Enterohaemorrhagic
	864	14	1.0	3131	1	V40561 Human thiazide-sen
	865	14	1.0	3138	1	V71041 Stat5-green floure
	866	14	1.0	3141	1	T47556 Human cytomegalovi
	867	14	1.0	3183	1	V09024 Homo sapiens 20q13
	868	14	1.0	3240	1	V48270 A. chrysogenum gam
c	869	14	1.0	3246	1	Q54170 B.stearothermophil
c	870	14	1.0	3252	1	Q31650 Bacillus caldotena
c	871	14	1.0	3303	1	Q14806 B.thuringiensis to
	872	14	1.0	3311	1	T70377 Cytohesin 1. Cytoh
c	873	14	1.0	3317	1	T97089 Bacillus stearothe
	874	14	1.0	3339	1	V61096 Mouse membrane typ
c	875	14	1.0	3350	1	T08553 Oncogene R-ras mut
	876	14	1.0	3358	1	V58005 Rat neurturin rece
c	877	14	1.0	3377	1	V64424 Mouse elf cDNA. Ne
c	878	14	1.0	3412	1	X25772 S.erythraea erythr
	879	14	1.0	3420	1	T75437 Mortierella alpina
	880	14	1.0	3423	1	X40183 Lung cancer associ
	881	14	1.0	3435	1	Q79746 Mycoplasma pirum a
	882	14	1.0	3445	1	Q48230 Acremonium chrysog
	883	14	1.0	3445	1	Q55405 A.chrysogenum beta
	884	14	1.0	3445	1	Q55406 A.chrysogenum beta
c	885	14	1.0	3451	1	V02308 Cell membrane prot
c	886	14	1.0	3456	1	T85397 Pseudomonas fluore
	887	14	1.0	3463	1	Q27180 Alkaline cellulase
c	888	14	1.0	3471	1	V16516 DNA encoding a Bac
	889	14	1.0	3474	1	Q39018 Sequence of pure m
c	890	14	1.0	3474	1	Q39018 Sequence of pure m
	891	14	1.0	3474	1	T74012 Maize optimised-B.
c	892	14	1.0	3474	1	T74012 Maize optimised-B.
	893	14	1.0	3474	1	V16191 Maize optimised DN
c	894	14	1.0	3474	1	V16191 Maize optimised DN
c	895	14	1.0	3478	1	V00291 Insecticidal prote
c	896	14	1.0	3484	1	V00395 Insecticidal gene
	897	14	1.0	3505	1	Q35270 Human GTA cDNA. De
c	898	14	1.0	3508	1	Q39020 Sequence of full l
c	899	14	1.0	3508	1	T74013 Full length maize
c	900	14	1.0	3508	1	V16192 Maize optimised DN
	901	14	1.0	3516	1	V71082 Green fluorescent
	902	14	1.0	3546	1	V71083 NFAT1-green fluore
c	903	14	1.0	3547	1	T01115 Expression vector
c	904	14	1.0	3547	1	V21771 V1R vaccination ve
c	905	14	1.0	3553	1	Q74208 Expression vector
c	906	14	1.0	3557	1	X04605 Maize genomic clon
c	907	14	1.0	3567	1	T47559 42K promoted cytom
	908	14	1.0	3569	1	T85905 Polygalacturonase
c	909	14	1.0	3603	1	T42217 Human TATA-binding
c	910	14	1.0	3603	1	T79595 TATA-binding prote
c	911	14	1.0	3610	1	V00669 Synthetic hepatiti
c	912	14	1.0	3635	1	V00125 Rat hexokinase II
c	913	14	1.0	3635	1	V00086 Rat hexokinase II
c	914	14	1.0	3647	1	V00159 Rat hexokinase I e
c	915	14	1.0	3647	1	V00085 Rat hexokinase I e
	916	14	1.0	3704	1	T59938 Phage resistance g
c	917	14	1.0	3733	1	V74849 Staphylococcus aur
	918	14	1.0	3748	1	Q23006 Actin gene (incl.
	919	14	1.0	3748	1	Q48535 Actin. Novel polyp
	920	14	1.0	3748	1	V20627 Sf9 alpha-mannosid
	921	14	1.0	3748	1	V16776 Sf9 alpha-mannosid
	922	14	1.0	3750	1	Q22203 A. chrysogenum act
	923	14	1.0	3756	1	T72684 Sugar biosynthesis
c	924	14	1.0	3771	1	Q20336 B.thuringiensis to
c	925	14	1.0	3771	1	Q30805 Toxin gene 33f2. N
c	926	14	1.0	3771	1	Q31411 Bacillus thuringie
c	927	14	1.0	3771	1	Q32161 BT toxin 33F2 Nema
c	928	14	1.0	3771	1	Q30937 BT toxin 33F2. New
c	929	14	1.0	3771	1	Q51689 Bacillus thuringie
c	930	14	1.0	3771	1	Q94055 Strain 33f2 DNA. D
c	931	14	1.0	3771	1	T60071 33F2 toxin coding
	932	14	1.0	3796	1	T93499 Xenopus frog prote
	933	14	1.0	3822	1	T84151 DNA encoding a mer
	934	14	1.0	3870	1	T12292 Phospholipase C-ga
c	935	14	1.0	3877	1	V02209 cDNA of leaderless
	936	14	1.0	3893	1	T12293 Phospholipase C-ga
c	937	14	1.0	3895	1	V52334 Streptococcus pneu
c	938	14	1.0	3896	1	X05816 Mouse pheromone re
	939	14	1.0	3919	1	V10355 Human tolloid-like
	940	14	1.0	3932	1	Q64112 cryET5 gene. Isola
	941	14	1.0	3934	1	T68434 CryET5 gene. Bacil
	942	14	1.0	3934	1	T95051 DNA encoding Bacil
	943	14	1.0	3934	1	V83927 DNA encoding a Cry
c	944	14	1.0	3955	1	V15181 Human serrate 2 en
	945	14	1.0	4000	1	T86166 Nucleotide sequenc
	946	14	1.0	4029	1	X13235 Enterococcus faeca
c	947	14	1.0	4075	1	T47557 42K promoted cytom
	948	14	1.0	4166	1	N90528 DNA sequence encod
c	949	14	1.0	4200	1	Q48652 43 kDa/156 kDa non
c	950	14	1.0	4200	1	Q45166 Sequence of precur
c	951	14	1.0	4200	1	Q98503 Rabbit 97 kDa dyst
c	952	14	1.0	4200	1	T97316 Rabbit (156 kDa) d
c	953	14	1.0	4239	1	V74644 Staphylococcus aur
	954	14	1.0	4239	1	X13387 Enterococcus faeca
c	955	14	1.0	4260	1	T47528 H6 promoted cytome
	956	14	1.0	4268	1	T00052 Hepatitis GB virus
c	957	14	1.0	4278	1	V52286 Streptococcus pneu
	958	14	1.0	4299	1	V03310 Pyrolobus fumarius
	959	14	1.0	4300	1	Q25812 Clone 45-A. Mammal
c	960	14	1.0	4315	1	V63754 Human JAGGED2 cDNA
c	961	14	1.0	4328	1	V21684 Vector plasmid CMV
c	962	14	1.0	4328	1	X24808 Vector CMVkm2. Lip
	963	14	1.0	4330	1	V26524 Plasmid pTLP2 enco
c	964	14	1.0	4344	1	Q56782 Insecticidal toxin
c	965	14	1.0	4344	1	V99986 Nucleotide sequenc
c	966	14	1.0	4373	1	T72719 Pyruvate:flavodoxi
c	967	14	1.0	4395	1	V65398 DNA encoding an an
c	968	14	1.0	4432	1	Q74206 Expression vector
c	969	14	1.0	4432	1	T01113 Expression vector
c	970	14	1.0	4453	1	T69890 Human cyclin D1-hu
c	971	14	1.0	4453	1	V54118 Human cyclin D1/cy
c	972	14	1.0	4483	1	T40091 Human Serrate-2 (H
c	973	14	1.0	4540	1	T69891 Human cyclin D1-hu
c	974	14	1.0	4540	1	V54119 Human cyclin D1/cy
	975	14	1.0	4575	1	N91465 Drosophila melanog
c	976	14	1.0	4588	1	V02185 Murine type C lect
c	977	14	1.0	4590	1	N60472 Sequence encoding
c	978	14	1.0	4594	1	T47533 CMV gB transmembra
c	979	14	1.0	4594	1	T47535 CMV gB transmembra
c	980	14	1.0	4621	1	T69889 Human cyclin D1-hu
c	981	14	1.0	4621	1	V54117 Human cyclin D1/cy
	982	14	1.0	4700	1	V30461 Soybean seed coat

c 983	14	1.0	4767	1	V21648	AAV4 genome. Adeno
c 984	14	1.0	4768	1	T47531	H6 promoted cytome
c 985	14	1.0	4771	1	V02186	Human type C lecti
c 986	14	1.0	4809	1	Q62185	pAQ1 plasmid fragm
c 987	14	1.0	4818	1	V21686	Vector plasmid CMV
c 988	14	1.0	4832	1	V74500	Staphylococcus aur
989	14	1.0	4839	1	Q06827	Alpha amylase pull
c 990	14	1.0	4864	1	Q74207	Expression vector
c 991	14	1.0	4864	1	T01114	Expression vector
c 992	14	1.0	4864	1	V21737	V1Jneo sequence us
c 993	14	1.0	4881	1	V63438	Feline herpesvirus
c 994	14	1.0	4909	1	T47558	42K promoted cytom
c 995	14	1.0	4912	1	X08423	Recombinant vector
c 996	14	1.0	4919	1	Q29260	Human calcium chan
c 997	14	1.0	4928	1	T32656	Plasmid encoding h
c 998	14	1.0	4942	1	X00461	Human type VI aden
c 999	14	1.0	4956	1	X13228	Enterococcus faeca
c1000	14	1.0	4973	1	V58289	S. pyogenes SP-55-

ALIGNMENTS

RESULT 1
X13598
ID X13598 standard; DNA; 965 BP.
AC X13598;
DT 19-MAR-1999 (first entry)
DE Enterococcus faecalis genome contig SEQ ID NO:661.
KW Enterococcus faecalis; contig; detection; Enterococcal infection;
KW vaccine; attenuation; computer readable medium; ds.
OS Enterococcus faecalis.
PN WO9850555-A2.
PD 12-NOV-1998.
PF 04-MAY-1998; U08985.
PR 14-NOV-1997; US-066009.
PR 06-MAY-1997; US-044031.
PR 16-MAY-1997; US-046655.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Barash SC, Dillon PJ, Kunsch CA;
DR WPI; 99-045171/04.
PT New isolated Enterococcus faecalis polynucleotides and polypeptides
PT - used to develop products for the detection of Enterococcus and for
PT use in vaccines for prevention or attenuation of Enterococcus
PT infection.
PS Claim 1; Page 1907; 2084pp; English.
CC A computer readable medium has been developed which has recorded on it
CC 982 nucleotide sequences isolated from the Enterococcus faecalis genome.
CC X12938 to X13919 represent these nucleotide sequences which are primary
CC nucleotide sequences, also known as contigs. The computer-based system
CC can identify fragments of the Enterococcus faecalis genome with
CC commercial importance. The products can be used to detect the presence
CC of Enterococcus faecalis in samples. They can also be used for
CC diagnosing Enterococcal infection in an animal and monitoring
CC progression of disease, and for identifying agents which can be used to
CC modulate the growth or pathogenicity of Enterococcus faecalis, or
CC another related organism, in vivo or in vitro. In particular the
CC polypeptides encoded by the Enterococcus faecalis nucleotide sequences
CC can be used in vaccines to prevent or attenuate an Enterococcal
CC infection.
SQ Sequence 965 BP; 288 A; 173 C; 133 G; 367 T;

Query Match 1.3%; Score 18; DB 1; Length 965;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      93 caaaaaagaagcatcctt 110
           ||||||||||||||||||
Db     197 CAAAAAAGAAGCATCCTT 214
```

RESULT 2
V58939
ID V58939 standard; DNA; 9960 BP.
AC V58939;
DT 15-FEB-1999 (first entry)
DE Mycobacterium smegmatis embCAB operon.
KW Drug resistance; antibiotic resistance; antimycobacterial;
KW ethambutol; embCAB operon; infection; vaccine; therapy; ds.
OS Mycobacterium smegmatis.
PN WO9841533-A1.
PD 24-SEP-1998.
PF 16-MAR-1998; U05128.
PR 20-MAR-1997; US-822586.
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
PI Jacobs WR, Musser J, Telenti A;
DR WPI; 98-521160/44.
DR P-PSDB; W73055-57.
PT Wild type and mutated sequences of Mycobacterium embCAB operon -
PT useful to e.g. identify ethambutol-resistant mycobacterial strains
PT and produce antisense sequences to treat mycobacterial infections
PS Disclosure; Fig 6A-I; 62pp; English.
CC This is the DNA sequence of the Mycobacterium smegmatis embCAB
CC operon, which determines resistance to the antimycobacterial drug
CC ethambutol (EMB). It includes the embA, embC and embb genes that
CC encode proteins (see W73052-54) which are the target of action of
CC M. smegmatis for EMB. To identify genes conferring EMB resistance,
CC a genomic library from a high level EMB-resistant mutant of M.
CC smegmatis was introduced into wild-type M. smegmatis mc2155. Four
CC overlapping cosmids were identified which conferred a resistant
CC phenotype. The minimum size fragment capable of conferring EMB
CC resistance was 9 kb (pIMM99). pIMM99 plus 7 kb upstream M.
CC smegmatis sequence was dequences revelaing 3 homologous open
CC reading frames (embC, embB, embB) and 4 additional potential coding
CC regions. Wild-type and mutated embCAB nucleic acid sequences are
CC useful as probes used in the diagnosis of drug-resistant
CC mycobacteria or to determine the susceptibility of mycobacteria to
CC EMB. The nucleic acids are also useful in the treatment of
CC mycobacterial infections; anti-DNA or anti-RNA sequences can be
CC administered to inhibit embCAB operon mRNA activity (claimed). The
CC invention additionally provides for the use of embCAM operon
CC nucleic acid sequences as vaccines, or to improve existing
CC vaccines.
SQ Sequence 9960 BP; 1389 A; 3592 C; 3360 G; 1618 T;

Query Match 1.3%; Score 18; DB 1; Length 9960;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy     401 acggctacatcctgacca 418
           ||||||||||||||||||
Db     956 ACGGCTACATCCTGACCA 973
```

RESULT 3
V58938
ID V58938 standard; DNA; 10095 BP.
AC V58938;
DT 15-FEB-1999 (first entry)
DE Mycobacterium tuberculosis embCAB operon.
KW Drug resistance; antibiotic resistance; antimycobacterial;
KW ethambutol; embCAB operon; infection; vaccine; therapy;
KW tuberculosis; ds.
OS Mycobacterium tuberculosis.
PN WO9841533-A1.
PD 24-SEP-1998.
PF 16-MAR-1998; U05128.
PR 20-MAR-1997; US-822586.
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
PI Jacobs WR, Musser J, Telenti A;
DR WPI; 98-521160/44.
DR P-PSDB; W73052-54.
PT Wild type and mutated sequences of Mycobacterium embCAB operon -
PT useful to e.g. identify ethambutol-resistant mycobacterial strains

```
PT   and produce antisense sequences to treat mycobacterial infections
PS   Disclosure; Fig 4A-I; 62pp; English.
CC   This is the DNA sequence of the Mycobacterium tuberculosis embCAB
CC   operon, which determines resistance to the antimycobacterial drug
CC   ethambutol (EMB).  It includes the embA, embC and embb genes
CC   that encode proteins (see W73052-54) which are the target of
CC   action of M. tuberculosis for EMB.  Wild-type and mutated embCAB
CC   nucleic acid sequences are useful e.g. as probes used in the
CC   diagnosis of drug-resistant mycobacteria or to determine the
CC   susceptibility of mycobacteria to EMB.  The nucleic acids are also
CC   useful in the treatment of mycobacterial infections; anti-DNA or
CC   anti-RNA sequences can be administered to inhibit embCAB operon
CC   mRNA activity (claimed).  The invention additionally provides for
CC   the use of embCAM operon nucleic acid sequences as vaccines, or
CC   to improve existing vaccines.
SQ   Sequence   10095 BP;    1469 A;    3475 C;    3370 G;    1780 T;

  Query Match             1.3%;  Score 18;  DB 1;  Length 10095;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    401 acggctacatcctgacca 418
          ||||||||||||||||||
Db   1031 ACGGCTACATCCTGACCA 1048


RESULT   4
T19263
ID   T19263 standard; cDNA to mRNA; 196 BP.
AC   T19263;
DT   28-JUN-1996  (first entry)
DE   Human gene signature HUMGS00280.
KW   Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW   human; cloning; mapping; non-biased library; diagnosis; detection;
KW   cell typing; abnormal cell function; ss.
OS   Homo sapiens.
PN   WO9514772-A1.
PD   01-JUN-1995.
PF   11-NOV-1994; J01916.
PR   12-NOV-1993; JP-355504.
PA   (MATS/) MATSUBARA K.
PA   (OKUB/) OKUBO K.
PI   Matsubara K,  Okubo K;
DR   WPI; 95-206931/27.
PT   Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT   for diagnosis of abnormal cell function, by preparing cDNA that
PT   reflects relative abundance of corresp. mRNA in specific human
PT   tissues
PS   Claim 1; Page 345; 2245pp; Japanese.
CC   A single-stranded DNA (or its complementary strand or the corresp.
CC   double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC   given in T19001-T26837 and which is able to hybridise to part of
CC   human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC   sequences were obtained from 3'-directed cDNA libraries prepared
CC   from various human tissues; synthesis of cDNA was initiated from the
CC   3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC   untranslated sequence is unique to a particular mRNA species, almost
CC   all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC   is constructed so as to reflect accurately the relative abundance of
CC   different mRNAs in the particular tissue from which it was derived.
CC   The appearance frequency of a given GS in a cDNA library can be
CC   determined (esp. using primers and probes derived from the GS
CC   sequences) as a means of diagnosing abnormal cell function or for
CC   recognising different cell types.
SQ   Sequence   196 BP;    59 A;    55 C;    34 G;    48 T;

  Query Match             1.2%;  Score 17;  DB 1;  Length 196;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    709 accgacgttgccatcaa 725
          |||||||||||||||||
Db     64 ACCGACGTTGCCATCAA 80


RESULT   5
V31989/c
ID   V31989 standard; DNA; 229 BP.
AC   V31989;
DT   25-SEP-1998  (first entry)
DE   BS106 polynucleotide clone 1662885 (i).
KW   ss; human; BS106; breast tissue gene; breast cancer; detection marker.
OS   Homo sapiens.
PN   WO9818945-A1.
PD   07-MAY-1998.
PF   31-OCT-1997; U19836.
PR   31-OCT-1996; US-742067.
PA   (ABBO ) ABBOTT LAB.
PI   Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN,
PI   Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD,
PI   Roberts-Rapp L, Russell JC, Stroupe SD;
DR   WPI; 98-272234/24.
PT   Detecting BS106 gene products - useful for developing products for
PT   detecting, staging, preventing, treating or determining
PT   predisposition to e.g. breast cancer
PS   Claim 1; Page 88; 114pp; English.
CC   BS106 is a breast tissue gene with which breast cancer and related
CC   diseases are associated.  The BS106 polynucleotides V31989-V31993 can be
CC   detected by BS106 specific polynucleotides or complements acting as
CC   useful markers for detection methods.  The products and methods can be
CC   used for detecting, diagnosing, staging,  preventing or treating, or
CC   determining predisposition to diseases or conditions of the breast such
CC   as breast cancer.
SQ   Sequence   229 BP;    43 A;    68 C;    50 G;    62 T;

  Query Match             1.2%;  Score 17;  DB 1;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    381 gggcttcatcatcagca 397
          |||||||||||||||||
Db    187 GGGCTTCATCATCAGCA 171


RESULT   6
V31990/c
ID   V31990 standard; DNA; 308 BP.
AC   V31990;
DT   25-SEP-1998  (first entry)
DE   BS106 polynucleotide clone 893988.
KW   ss; human; BS106; breast tissue gene; breast cancer; detection marker.
OS   Homo sapiens.
PN   WO9818945-A1.
PD   07-MAY-1998.
PF   31-OCT-1997; U19836.
PR   31-OCT-1996; US-742067.
PA   (ABBO ) ABBOTT LAB.
PI   Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN,
PI   Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD,
PI   Roberts-Rapp L, Russell JC, Stroupe SD;
DR   WPI; 98-272234/24.
PT   Detecting BS106 gene products - useful for developing products for
PT   detecting, staging, preventing, treating or determining
PT   predisposition to e.g. breast cancer
PS   Claim 1; Page 89; 114pp; English.
CC   BS106 is a breast tissue gene with which breast cancer and related
CC   diseases are associated.  The BS106 polynucleotides V31989-V31993 can be
CC   detected by BS106 specific polynucleotides or complements acting as
CC   useful markers for detection methods.  The products and methods can be
CC   used for detecting, diagnosing, staging,  preventing or treating, or
CC   determining predisposition to diseases or conditions of the breast such
CC   as breast cancer.
SQ   Sequence   308 BP;    63 A;    94 C;    65 G;    86 T;
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  Query Match             1.2%;  Score 17;  DB 1;  Length 308;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    381 gggcttcatcatcagca 397
          |||||||||||||||||
Db    174 GGGCTTCATCATCAGCA 158


RESULT   7
V31992/c
ID   V31992 standard; DNA; 482 BP.
AC   V31992;
DT   25-SEP-1998  (first entry)
DE   BS106 polynucleotide consensus sequence.
KW   ss; human; BS106; breast tissue gene; breast cancer; detection marker.
OS   Homo sapiens.
PN   WO9818945-A1.
PD   07-MAY-1998.
PF   31-OCT-1997; U19836.
PR   31-OCT-1996; US-742067.
PA   (ABBO ) ABBOTT LAB.
PI   Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN,
PI   Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD,
PI   Roberts-Rapp L, Russell JC, Stroupe SD;
DR   WPI; 98-272234/24.
PT   Detecting BS106 gene products - useful for developing products for
PT   detecting, staging, preventing, treating or determining
PT   predisposition to e.g. breast cancer
PS   Claim 1; Page 88; 114pp; English.
CC   BS106 is a breast tissue gene with which breast cancer and related
CC   diseases are associated.  The BS106 polynucleotides V31989-V31993 can be
CC   detected by BS106 specific polynucleotides or complements acting as
CC   useful markers for detection methods.  The products and methods can be
CC   used for detecting, diagnosing, staging,  preventing or treating, or
CC   determining predisposition to diseases or conditions of the breast such
CC   as breast cancer.
SQ   Sequence   482 BP;    109 A;    136 C;    90 G;    145 T;


  Query Match             1.2%;  Score 17;  DB 1;  Length 482;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    381 gggcttcatcatcagca 397
          |||||||||||||||||
Db    187 GGGCTTCATCATCAGCA 171


RESULT   8
X00704/c
ID   X00704 standard; DNA; 489 BP.
AC   X00704;
DT   25-MAR-1999  (first entry)
DE   Human secreted protein gene 34 clone HMQAJ64.
KW   Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW   diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW   developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW   immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW   inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW   cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW   osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW   endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS   Homo sapiens.
PN   WO9842738-A1.
PD   01-OCT-1998.
PF   19-MAR-1998; U05311.
PR   30-MAY-1997; US-050937.
PR   21-MAR-1997; US-041276.
PR   21-MAR-1997; US-041277.
PR   21-MAR-1997; US-041281.
PR   21-MAR-1997; US-042344.
PR   30-MAY-1997; US-048069.
PR   30-MAY-1997; US-048094.
PR   30-MAY-1997; US-048095.
PR   30-MAY-1997; US-048096.
PR   30-MAY-1997; US-048099.
PR   30-MAY-1997; US-048131.
PR   30-MAY-1997; US-048135.
PR   30-MAY-1997; US-048154.
PR   30-MAY-1997; US-048160.
PR   30-MAY-1997; US-048186.
PR   30-MAY-1997; US-048187.
PR   30-MAY-1997; US-048188.
PR   30-MAY-1997; US-048350.
PR   30-MAY-1997; US-048351.
PR   30-MAY-1997; US-048352.
PR   30-MAY-1997; US-048355.
PR   05-AUG-1997; US-054804.
PA   (HUMA-) HUMAN GENOME SCI INC.
PI   Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA,
PI   Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS,
PI   Rosen CA, Ruben SM, Shi Y, Young P;
DR   WPI; 99-070066/06.
DR   P-PSDB; W67900.
PT   New isolated human genes and the secreted polypeptides they encode -
PT   useful for diagnosis and treatment of e.g. cancers, neurological
PT   disorders, immune diseases, inflammation or blood disorders
PS   Claim 1; Page 254; 385pp; English.
CC   This sequence represents a nucleic acid molecule which encodes a secreted
CC   human protein.  The gene number, and the clone it is derived from, are
CC   detailed in the descriptor line.  The gene can be used to generate fusion
CC   proteins by linking to the gene to a human immunoglobulin Fc portion
CC   (e.g. X00602) for increasing the stability of the fused protein as
CC   compared to the human protein only.
CC   The invention relates to 87 novel genes and their fragments (nucleic acid
CC   sequences: X00611-X00724; amino acid sequences W67807-W68004) which
CC   are useful for preventing, treating or ameliorating  medical conditions
CC   e.g. by protein or gene therapy.  Also, pathological conditions can be
CC   diagnosed by determining the amount of the new polypeptides in a sample
CC   or by determining the presence of mutations in the new polynucleotides.
CC   Specific uses are described for each of the 87 polynucleotides, based on
CC   which tissues they are most highly expressed in (see X00611 for described
CC   uses).
SQ   Sequence   489 BP;    124 A;    134 C;    91 G;    140 T;


  Query Match             1.2%;  Score 17;  DB 1;  Length 489;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    381 gggcttcatcatcagca 397
          |||||||||||||||||
Db    181 GGGCTTCATCATCAGCA 165


RESULT   9
X00644/c
ID   X00644 standard; DNA; 489 BP.
AC   X00644;
DT   25-MAR-1999  (first entry)
DE   Human secreted protein gene 34 clone HMQAJ64.
KW   Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW   diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW   developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW   immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW   inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW   cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW   osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW   endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS   Homo sapiens.
PN   WO9842738-A1.
PD   01-OCT-1998.
PF   19-MAR-1998; U05311.
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PR   30-MAY-1997; US-050937.
PR   21-MAR-1997; US-041276.
PR   21-MAR-1997; US-041277.
PR   21-MAR-1997; US-041281.
PR   21-MAR-1997; US-042344.
PR   30-MAY-1997; US-048069.
PR   30-MAY-1997; US-048094.
PR   30-MAY-1997; US-048095.
PR   30-MAY-1997; US-048096.
PR   30-MAY-1997; US-048099.
PR   30-MAY-1997; US-048131.
PR   30-MAY-1997; US-048135.
PR   30-MAY-1997; US-048154.
PR   30-MAY-1997; US-048160.
PR   30-MAY-1997; US-048186.
PR   30-MAY-1997; US-048187.
PR   30-MAY-1997; US-048188.
PR   30-MAY-1997; US-048350.
PR   30-MAY-1997; US-048351.
PR   30-MAY-1997; US-048352.
PR   30-MAY-1997; US-048355.
PR   05-AUG-1997; US-054804.
PA   (HUMA-) HUMAN GENOME SCI INC.
PI   Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA,
PI   Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS,
PI   Rosen CA, Ruben SM, Shi Y, Young P;
DR   WPI; 99-070066/06.
DR   P-PSDB; W67840.
PT   New isolated human genes and the secreted polypeptides they encode -
PT   useful for diagnosis and treatment of e.g. cancers, neurological
PT   disorders, immune diseases, inflammation or blood disorders
PS   Claim 1; Page 198; 385pp; English.
CC   This sequence represents a nucleic acid molecule which encodes a secreted
CC   human protein.  The gene number, and the clone it is derived from, are
CC   detailed in the descriptor line.  The gene can be used to generate fusion
CC   proteins by linking to the gene to a human immunoglobulin Fc portion
CC   (e.g. X00602) for increasing the stability of the fused protein as
CC   compared to the human protein only.
CC   The invention relates to 87 novel genes and their fragments (nucleic acid
CC   sequences: X00611-X00724; amino acid sequences W67807-W68004) which
CC   are useful for preventing, treating or ameliorating  medical conditions
CC   e.g. by protein or gene therapy.  Also, pathological conditions can be
CC   diagnosed by determining the amount of the new polypeptides in a sample
CC   or by determining the presence of mutations in the new polynucleotides.
CC   Specific uses are described for each of the 87 polynucleotides, based on
CC   which tissues they are most highly expressed in (see X00611 for described
CC   uses).
SQ   Sequence   489 BP;    125 A;    134 C;    87 G;    143 T;


  Query Match             1.2%;  Score 17;  DB 1;  Length 489;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    381 gggcttcatcatcagca 397
          |||||||||||||||||
Db    178 GGGCTTCATCATCAGCA 162


RESULT  10
V31993/c
ID   V31993 standard; DNA; 553 BP.
AC   V31993;
DT   25-SEP-1998  (first entry)
DE   BS106 polynucleotide clone 1662885 (ii).
KW   ss; human; BS106; breast tissue gene; breast cancer; detection marker.
OS   Homo sapiens.
PN   WO9818945-A1.
PD   07-MAY-1998.
PF   31-OCT-1997; U19836.
PR   31-OCT-1996; US-742067.
PA   (ABBO ) ABBOTT LAB.
PI   Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN,
PI   Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD,
PI   Roberts-Rapp L, Russell JC, Stroupe SD;
DR   WPI; 98-272234/24.
PT   Detecting BS106 gene products - useful for developing products for
PT   detecting, staging, preventing, treating or determining
PT   predisposition to e.g. breast cancer
PS   Claim 1; Page 90; 114pp; English.
CC   BS106 is a breast tissue gene with which breast cancer and related
CC   diseases are associated.  The BS106 polynucleotides V31989-V31993 can be
CC   detected by BS106 specific polynucleotides or complements acting as
CC   useful markers for detection methods.  The products and methods can be
CC   used for detecting, diagnosing, staging,  preventing or treating, or
CC   determining predisposition to diseases or conditions of the breast such
CC   as breast cancer.
SQ   Sequence   553 BP;    159 A;    144 C;    101 G;    148 T;


  Query Match             1.2%;  Score 17;  DB 1;  Length 553;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    381 gggcttcatcatcagca 397
          |||||||||||||||||
Db    201 GGGCTTCATCATCAGCA 185


RESULT  11
V29521
ID   V29521 standard; cDNA; 732 BP.
AC   V29521;
DT   13-OCT-1998  (first entry)
DE   Homo sapiens LexA-PS-1 fusion protein cDNA.
KW   fusion protein; LexA; PS-1; presenilin; presenilin-1; PSP-1;
KW   Alzheimer's disease; serine protease; neurodegeneration;
KW   predisposition; diagnosis; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             2. .523
FT                   /*tag= a
FT                   /product= LexA-PS- fusion protein
PN   EP-828003-A2.
PD   11-MAR-1998.
PF   26-AUG-1997; 306501.
PR   13-DEC-1996; US-032875.
PR   06-SEP-1996; US-025436.
PR   25-OCT-1996; US-027873.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PI   Browne MJ, Clinkenbeard HE, Creasy CL, Karran EH,
PI   Livi GP, Southan CD;
DR   WPI; 98-161101/15.
DR   P-PSDB; W56766.
PT   Nucleic acids encoding human serum protease protein(s) - used for
PT   diagnosing pre-disposition to Alzheimer's disease, etc.
PS   Example 2; Page 17; 65pp; English.
CC   The sequence is that encoding a LexA-PS-1 fusion protein which
CC   was used in the cloning of PSP-1. This can be used to identify
CC   modulators of serine protease activity and also to diagnose a
CC   condition associated with lack of one of the serine proteases
CC   or a genetic predisposition to neurodegeneration in a patient,
CC   preferably predisposition to Alzheimer's disease.
SQ   Sequence   732 BP;    197 A;    177 C;    184 G;    174 T;


  Query Match             1.2%;  Score 17;  DB 1;  Length 732;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    820 atctcctttgccatccc 836
          |||||||||||||||||
Db    131 ATCTCCITTGCCATCCC 147
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RESULT  12
V28875/c
ID   V28875 standard; cDNA; 1029 BP.
AC   V28875;
DT   28-AUG-1998  (first entry)
DE   Candida antartica lipase B clb gene coding region.
KW   Host cell; neutral metalloprotease; alkaline protease; lipase B;
KW   clb gene; ss.
OS   Candida antarctica.
PN   WO9812300-A1.
PD   26-MAR-1998.
PF   19-SEP-1997; DK0397.
PR   19-SEP-1996; DK-001024.
PA   (NOVO ) NOVO-NORDISK AS.
PI   Lehmbeck J;
DR   WPI; 98-217244/19.
PT   New modified host cells - are modified to express reduced levels of
PT   metallo-protease and alkaline protease, used to increase production
PT   of heterologous protein products
PS   Example 2; Page 32; 49pp; English.
CC   This polynucleotide comprises the coding region of the lipase B
CC   clb gene of Candida antarctica.  The clb gene was isolated from a
CC   C. antarctica genomic library using probes (see V28873-74) based on
CC   the N-terminal amino acid sequence (see W57238) of lipase B.  The
CC   gene was expressed in Aspergillus oryzae IFO 4177 and JaL228, the
CC   latter having both the alkaline protease alp gene (see V28870) and
CC   neutral metalloprotease I NpI gene (see V28869) deleted.  CLB
CC   activity reached 1041 LU/g after 93 hr fermentation of JaL228,
CC   compared with 575 LU/g with IFO 4177.  The invention provides
CC   metalloprotease- and alkaline protease-deleted yeast and fungal
CC   host cells and their use for improved production of heterologous
CC   protein products.
SQ   Sequence   1029 BP;    183 A;    376 C;    259 G;    211 T;


  Query Match             1.2%;  Score 17;  DB 1;  Length 1029;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      58 ggctgcgaaaaggcagg 74
           |||||||||||||||||
Db     110 GGCTGCGAAAAGGCAGG 94


RESULT  13
V84576/c
ID   V84576 standard; DNA; 1348 BP.
AC   V84576;
DT   01-MAR-1999  (first entry)
DE   Human secreted protein gene 166 clone HCEQA68.
KW   Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW   diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW   developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW   immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW   inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW   cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW   osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW   endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS   Homo sapiens.
PN   WO9854963-A2.
PD   10-DEC-1998.
PF   04-JUN-1998; U11422.
PR   18-DEC-1997; US-070923.
PR   06-JUN-1997; US-048877.
PR   06-JUN-1997; US-048881.
PR   06-JUN-1997; US-048884.
PR   06-JUN-1997; US-048893.
PR   06-JUN-1997; US-048896.
PR   06-JUN-1997; US-048899.
PR   06-JUN-1997; US-048915.
PR   06-JUN-1997; US-048949.
PR   06-JUN-1997; US-048964.
PR   06-JUN-1997; US-048972.
PR   06-JUN-1997; US-049020.
PR   06-JUN-1997; US-049375.
PR   05-SEP-1997; US-057628.
PR   05-SEP-1997; US-057635.
PR   05-SEP-1997; US-057644.
PR   05-SEP-1997; US-057647.
PR   05-SEP-1997; US-057650.
PR   05-SEP-1997; US-057661.
PR   05-SEP-1997; US-057667.
PR   05-SEP-1997; US-057761.
PR   05-SEP-1997; US-057764.
PR   05-SEP-1997; US-057770.
PR   05-SEP-1997; US-057775.
PR   05-SEP-1997; US-057778.
PR   06-JUN-1997; US-048875.
PR   06-JUN-1997; US-048878.
PR   06-JUN-1997; US-048882.
PR   06-JUN-1997; US-048885.
PR   06-JUN-1997; US-048894.
PR   06-JUN-1997; US-048897.
PR   06-JUN-1997; US-048900.
PR   06-JUN-1997; US-048916.
PR   06-JUN-1997; US-048962.
PR   06-JUN-1997; US-048970.
PR   06-JUN-1997; US-048974.
PR   06-JUN-1997; US-049373.
PR   05-SEP-1997; US-057584.
PR   05-SEP-1997; US-057629.
PR   05-SEP-1997; US-057642.
PR   05-SEP-1997; US-057645.
PR   05-SEP-1997; US-057648.
PR   05-SEP-1997; US-057651.
PR   05-SEP-1997; US-057662.
PR   05-SEP-1997; US-057668.
PR   05-SEP-1997; US-057762.
PR   05-SEP-1997; US-057765.
PR   05-SEP-1997; US-057771.
PR   05-SEP-1997; US-057776.
PR   06-JUN-1997; US-048876.
PR   06-JUN-1997; US-048880.
PR   06-JUN-1997; US-048883.
PR   06-JUN-1997; US-048892.
PR   06-JUN-1997; US-048895.
PR   06-JUN-1997; US-048898.
PR   06-JUN-1997; US-048901.
PR   06-JUN-1997; US-048917.
PR   06-JUN-1997; US-048963.
PR   06-JUN-1997; US-048971.
PR   06-JUN-1997; US-049019.
PR   06-JUN-1997; US-049374.
PR   05-SEP-1997; US-057627.
PR   05-SEP-1997; US-057634.
PR   05-SEP-1997; US-057643.
PR   05-SEP-1997; US-057646.
PR   05-SEP-1997; US-057649.
PR   05-SEP-1997; US-057654.
PR   05-SEP-1997; US-057666.
PR   05-SEP-1997; US-057760.
PR   05-SEP-1997; US-057763.
PR   05-SEP-1997; US-057769.
PR   05-SEP-1997; US-057774.
PR   05-SEP-1997; US-057777.
PA   (HUMA-) HUMAN GENOME SCI INC.
PI   Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA,
PI   Fan P, Feng P, Ferrie AM, Fischer CL, Florence C,
PI   Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW,
PI   Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM,
PI   Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
DR   WPI; 99-059865/05.
DR   P-PSDB; W88699.
PT   New isolated human genes and the secreted polypeptides they encode -
PT   useful for diagnosis and treatment of e.g. cancers, neurological
PT   disorders, immune diseases, inflammation or blood disorders
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PS   Claim 4; Page 427-428; 772pp; English.
CC   The invention relates to nucleic acid sequences (V84411 to V84633)
CC   encoding human secreted proteins (W88534 to W88756). The secreted protein
CC   gene sequences are deposited with the ATCC under deposit numbers ATCC
CC   97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,
CC   209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host
CC   cells comprising recombinant vectors containing the nucleic acid
CC   sequences are used for the recombinant production of the secreted
CC   proteins. The polynucleotide and amino acid sequences are useful for are
CC   useful for preventing, treating or ameliorating medical conditions e.g.
CC   by protein or gene therapy. Pathological conditions can be also diagnosed
CC   by determining the amount of the new polypeptides in a sample or by
CC   determining the presence of mutations in the new polynucleotides.
CC   Specific uses are described for each of the polynucleotides, based on
CC   which tissues they are most highly expressed in, and include developing
CC   products for the diagnosis or treatment of cancer, neurodegenerative
CC   disorders, developmental abnormalities and foetal deficiencies, blood
CC   disorders, tumours, leukemias, diseases of the immune system, autoimmune
CC   diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
CC   ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,
CC   restenosis, prostate diseases, obesity, disorders involving osteoclasts
CC   such as osteoporosis, arthritis or malignancies, diseases of testes, lung
CC   or thymus, digestive/endocrine disorders, infections and AIDS. The
CC   polypeptides are also useful for identifying their binding partners.
CC   The present sequence represents a gene encoding a human secreted protein
CC   (see descriptor line for gene number and clone identification).
SQ   Sequence   1348 BP;    286 A;    374 C;    388 G;    292 T;

  Query Match              1.2%;  Score 17;  DB 1;  Length 1348;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    641 tgaccgccggcatcgtg 657
          |||||||||||||||||
Db     24 TGACCGCCGGCATCGTG 8


RESULT  14
V29523
ID   V29523 standard; cDNA; 1503 BP.
AC   V29523;
DT   13-OCT-1998  (first entry)
DE   Homo sapiens PSP1 clone.
KW   PS-1; presenilin; presenilin-1; PSP-1; Alzheimer's disease;
KW   serine protease; neurodegeneration; predisposition; diagnosis; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             1. .1272
FT                   /*tag=  a
FT                   /product= PSP1 fragment
PN   EP-828003-A2.
PD   11-MAR-1998.
PF   26-AUG-1997; 306501.
PR   13-DEC-1996; US-032875.
PR   06-SEP-1996; US-025436.
PR   25-OCT-1996; US-027873.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PI   Browne MJ, Clinkenbeard HE, Creasy CL, Karran EH,
PI   Livi GP, Southan CD;
DR   WPI; 98-161101/15.
DR   P-PSDB; W56768.
PT   Nucleic acids encoding human serum protease protein(s) - used for
PT   diagnosing pre-disposition to Alzheimer's disease, etc.
PS   Example 2; Page 19-20; 65pp; English.
CC   The sequence is that of an isolated cDNA clone encoding at least
CC   part of the serine protease PSP1. This can be used to identify
CC   modulators of serine protease activity and also to diagnose a
CC   condition associated with lack of one of the serine proteases
CC   or a genetic predisposition to neurodegeneration in a patient,
CC   preferably predisposition to Alzheimer's disease.
SQ   Sequence   1503 BP;    329 A;    405 C;    448 G;    321 T;

  Query Match              1.2%;  Score 17;  DB 1;  Length 1503;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    820 atctcctttgccatccc 836
          |||||||||||||||||
Db    976 ATCTCCTTTGCCATCCC 992


RESULT  15
V29522
ID   V29522 standard; cDNA; 1787 BP.
AC   V29522;
DT   13-OCT-1998  (first entry)
DE   Homo sapiens PSP1 clone.
KW   PS-1; presenilin; presenilin-1; PSP-1; Alzheimer's disease;
KW   serine protease; neurodegeneration; predisposition; diagnosis; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             1. .972
FT                   /*tag=  a
FT                   /product= PSP1 fragment
PN   EP-828003-A2.
PD   11-MAR-1998.
PF   26-AUG-1997; 306501.
PR   13-DEC-1996; US-032875.
PR   06-SEP-1996; US-025436.
PR   25-OCT-1996; US-027873.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PI   Browne MJ, Clinkenbeard HE, Creasy CL, Karran EH,
PI   Livi GP, Southan CD;
DR   WPI; 98-161101/15.
DR   P-PSDB; W56767.
PT   Nucleic acids encoding human serum protease protein(s) - used for
PT   diagnosing pre-disposition to Alzheimer's disease, etc.
PS   Example 2; Page 18; 65pp; English.
CC   The sequence is that of an isolated cDNA clone encoding at least
CC   part of the serine protease PSP1. This can be used to identify
CC   modulators of serine protease activity and also to diagnose a
CC   condition associated with lack of one of the serine proteases
CC   or a genetic predisposition to neurodegeneration in a patient,
CC   preferably predisposition to Alzheimer's disease.
SQ   Sequence   1787 BP;    392 A;    480 C;    498 G;    417 T;

  Query Match              1.2%;  Score 17;  DB 1;  Length 1787;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    820 atctcctttgccatccc 836
          |||||||||||||||||
Db   1048 ATCTCCTTTGCCATCCC 1064


Search completed: April 14, 2000, 18:30:14
Job time: 5855 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 14, 2000, 18:26:45 ; Search time 83.3 Seconds
(without alignments)
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Title: US-09-388-090-3
Perfect score: 1395
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 214294 seqs, 59861574 residues

Word size : 0

Total number of hits satisfying chosen parameters: 428588

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_NA:*
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4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
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7: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	17	1.2	49377	2	US-08-764-233A-1	Sequence 1, Appli
c	2	16	1.1	76	6	PCT-US91-02942-27	Sequence 27, Appl
c	3	16	1.1	388	1	US-08-171-385-10	Sequence 10, Appl
c	4	16	1.1	894	2	US-08-534-910B-4	Sequence 4, Appli
	5	16	1.1	929	5	US-08-860-368B-4	Sequence 4, Appli
	6	16	1.1	1155	5	US-08-860-368B-19	Sequence 19, Appl
	7	16	1.1	1158	5	US-08-860-368B-1	Sequence 1, Appli
	8	16	1.1	1288	1	US-08-142-897-4	Sequence 4, Appli
c	9	16	1.1	1479	1	US-08-476-008-68	Sequence 68, Appl
c	10	16	1.1	1479	1	US-08-306-063-68	Sequence 68, Appl
c	11	16	1.1	1479	2	US-08-833-485-68	Sequence 68, Appl
	12	16	1.1	2061	1	US-08-204-656B-9	Sequence 9, Appli
	13	16	1.1	2061	1	US-08-470-702-5	Sequence 5, Appli
	14	16	1.1	2061	1	US-08-467-831-5	Sequence 5, Appli
	15	16	1.1	2157	3	US-08-132-990A-7	Sequence 7, Appli
	16	16	1.1	2157	6	PCT-US92-09382-7	Sequence 7, Appli
c	17	16	1.1	4474	1	US-08-480-547A-9	Sequence 9, Appli
c	18	16	1.1	4474	2	US-08-250-847B-9	Sequence 9, Appli
c	19	16	1.1	4474	4	US-08-463-949A-9	Sequence 9, Appli
c	20	16	1.1	4474	6	PCT-US94-06066-9	Sequence 9, Appli
c	21	16	1.1	5541	2	US-08-920-812-20	Sequence 20, Appl
c	22	16	1.1	5541	2	US-08-920-827-20	Sequence 20, Appl
c	23	16	1.1	5541	2	US-08-921-177-20	Sequence 20, Appl
c	24	16	1.1	5541	2	US-08-362-577C-20	Sequence 20, Appl
c	25	16	1.1	5541	3	US-08-920-828-20	Sequence 20, Appl
c	26	16	1.1	8378	6	PCT-US91-09055-1	Sequence 1, Appli
	27	16	1.1	9432	1	US-08-277-231A-1	Sequence 1, Appli
	28	16	1.1	9432	3	US-08-473-750-4	Sequence 4, Appli
	29	16	1.1	9432	4	US-08-477-326-4	Sequence 4, Appli
	30	16	1.1	14255	1	US-08-320-559-1	Sequence 1, Appli
	31	16	1.1	14255	1	US-08-327-392-1	Sequence 1, Appli
	32	16	1.1	14255	2	US-08-306-691B-55	Sequence 55, Appl
	33	16	1.1	14255	6	PCT-US94-04496-1	Sequence 1, Appli
	34	15	1.1	570	1	US-07-963-331D-2	Sequence 2, Appli
	35	15	1.1	573	1	US-07-963-331D-1	Sequence 1, Appli
	36	15	1.1	804	4	US-08-611-880-4	Sequence 4, Appli
c	37	15	1.1	1434	3	US-08-770-544-15	Sequence 15, Appl
c	38	15	1.1	1650	1	US-08-245-758-11	Sequence 11, Appl
c	39	15	1.1	1650	4	US-08-810-655A-1	Sequence 1, Appli
c	40	15	1.1	1650	6	PCT-US95-05134-11	Sequence 11, Appl
	41	15	1.1	1677	4	US-08-989-107-33	Sequence 33, Appl
c	42	15	1.1	1700	2	US-08-665-220-1	Sequence 1, Appli
c	43	15	1.1	1764	3	US-08-642-684-1	Sequence 1, Appli
	44	15	1.1	1767	1	US-08-399-646-1	Sequence 1, Appli
	45	15	1.1	1767	2	US-08-607-321-1	Sequence 1, Appli
	46	15	1.1	1767	3	US-08-961-240-1	Sequence 1, Appli
	47	15	1.1	1767	3	US-08-605-501-1	Sequence 3, Appli
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c	49	15	1.1	1806	4	US-08-980-060-1	Sequence 1, Appli
c	50	15	1.1	1930	1	US-07-982-112-1	Sequence 1, Appli
	51	15	1.1	1949	4	US-08-540-804-1	Sequence 1, Appli
	52	15	1.1	1949	4	US-08-218-265-1	Sequence 26, Appl
c	53	15	1.1	1988	2	US-08-469-202-26	Sequence 33, Appl
c	54	15	1.1	1988	4	US-08-484-434C-33	Sequence 25, Appl
c	55	15	1.1	2000	2	US-08-469-202-25	Sequence 32, Appl
c	56	15	1.1	2000	4	US-08-484-434C-32	Sequence 3, Appli
c	57	15	1.1	2021	1	US-07-882-925A-3	Sequence 3, Appli
c	58	15	1.1	2021	1	US-08-184-012C-3	Sequence 2, Appli
c	59	15	1.1	2082	3	US-08-785-310A-2	Sequence 6, Appli
	60	15	1.1	2092	6	PCT-US95-11808-6	Sequence 11, Appl
	61	15	1.1	2161	1	US-08-399-646-11	Sequence 11, Appl
	62	15	1.1	2161	2	US-08-607-321-11	Sequence 11, Appl
	63	15	1.1	2161	3	US-08-961-240-11	Sequence 11, Appl
	64	15	1.1	2161	3	US-08-605-501-11	Sequence 2, Appli
c	65	15	1.1	2216	4	US-08-666-082B-2	Sequence 1, Appli
c	66	15	1.1	2219	1	US-07-882-925A-1	Sequence 2, Appli
c	67	15	1.1	2219	1	US-07-882-925A-2	Sequence 1, Appli
c	68	15	1.1	2219	1	US-08-184-012C-1	Sequence 2, Appli
c	69	15	1.1	2219	1	US-08-184-012C-2	Sequence 1, Appli
c	70	15	1.1	2232	2	US-08-334-177-1	Sequence 1, Appli
c	71	15	1.1	2232	6	PCT-US95-13830-1	Sequence 7, Appli
c	72	15	1.1	2262	1	US-07-882-925A-7	Sequence 7, Appli
c	73	15	1.1	2262	1	US-08-184-012C-7	Sequence 3, Appli
	74	15	1.1	2325	3	US-08-714-677-3	Sequence 3, Appli
	75	15	1.1	2325	3	US-08-393-540-3	Sequence 3, Appli
	76	15	1.1	2325	3	US-08-714-537-3	Sequence 21, Appl
c	77	15	1.1	2352	3	US-08-889-909A-21	Sequence 1, Appli
	78	15	1.1	2471	1	US-08-152-271-1	Sequence 1, Appli
c	79	15	1.1	2631	2	US-08-510-215A-1	Sequence 1, Appli
c	80	15	1.1	2717	1	US-07-723-002C-1	Sequence 1, Appli
c	81	15	1.1	2749	2	US-08-265-628-1	Sequence 11, Appl
	82	15	1.1	3073	3	US-08-714-677-11	Sequence 11, Appl
	83	15	1.1	3073	3	US-08-393-540-11	Sequence 11, Appl
	84	15	1.1	3073	3	US-08-714-537-11	Sequence 1, Appli
	85	15	1.1	3098	1	US-08-447-500-1	Sequence 1, Appli
	86	15	1.1	3098	1	US-08-454-097-1	Sequence 1, Appli
	87	15	1.1	3098	2	US-08-447-408-1	Sequence 1, Appli
	88	15	1.1	3098	2	US-08-453-866-1	Sequence 1, Appli
	89	15	1.1	3252	4	US-08-809-740A-1	Sequence 4, Appli
	90	15	1.1	3252	4	US-08-809-740A-4	Sequence 1, Appli
c	91	15	1.1	3384	4	US-08-687-289A-1	Sequence 3, Appli
c	92	15	1.1	3459	4	US-08-980-060-3	Sequence 1, Appli
c	93	15	1.1	3535	3	US-08-618-408B-1	Sequence 7, Appli
	94	15	1.1	3684	2	US-08-448-170-7	Sequence 3, Appli
c	95	15	1.1	3809	1	US-08-485-588-3	Sequence 3, Appli
c	96	15	1.1	3809	2	US-08-484-565-3	Sequence 3, Appli
c	97	15	1.1	3809	3	US-08-480-751-3	Sequence 3, Appli
c	98	15	1.1	3809	4	US-08-943-986-3	Sequence 3, Appli
c	99	15	1.1	3809	5	US-08-353-784-3	

c 100	15	1.1	3921	4	US-08-567-375-3	Sequence 3, Appli
c 101	15	1.1	3921	4	US-08-587-680A-3	Sequence 3, Appli
c 102	15	1.1	4086	1	US-08-313-181-1	Sequence 1, Appli
c 103	15	1.1	4131	1	US-08-485-588-4	Sequence 4, Appli
c 104	15	1.1	4131	2	US-08-484-565-4	Sequence 4, Appli
c 105	15	1.1	4131	3	US-08-480-751-4	Sequence 4, Appli
c 106	15	1.1	4131	4	US-08-943-986-4	Sequence 4, Appli
c 107	15	1.1	4131	5	US-08-353-784-4	Sequence 4, Appli
108	15	1.1	4440	1	US-08-200-016-4	Sequence 4, Appli
c 109	15	1.1	5006	1	US-08-485-588-2	Sequence 2, Appli
c 110	15	1.1	5006	2	US-08-484-565-2	Sequence 2, Appli
c 111	15	1.1	5006	3	US-08-480-751-2	Sequence 2, Appli
c 112	15	1.1	5006	4	US-08-943-986-2	Sequence 2, Appli
c 113	15	1.1	5006	5	US-08-353-784-2	Sequence 2, Appli
c 114	15	1.1	5125	1	US-08-094-948A-4	Sequence 4, Appli
c 115	15	1.1	5125	6	PCT-US96-09319-4	Sequence 4, Appli
c 116	15	1.1	5275	1	US-08-485-588-1	Sequence 1, Appli
c 117	15	1.1	5275	2	US-08-484-565-1	Sequence 1, Appli
c 118	15	1.1	5275	3	US-08-480-751-1	Sequence 1, Appli
c 119	15	1.1	5275	4	US-08-943-986-1	Sequence 1, Appli
c 120	15	1.1	5275	5	US-08-353-784-1	Sequence 1, Appli
c 121	15	1.1	5992	3	US-08-475-891A-3	Sequence 3, Appli
c 122	15	1.1	6256	3	US-08-475-891A-1	Sequence 1, Appli
c 123	15	1.1	6256	4	US-08-567-375-1	Sequence 1, Appli
c 124	15	1.1	6256	4	US-08-587-680A-1	Sequence 1, Appli
c 125	15	1.1	7451	2	US-08-684-672-23	Sequence 23, Appl
c 126	15	1.1	8051	4	US-08-576-626A-2	Sequence 2, Appli
127	15	1.1	9493	4	US-08-639-857-23	Sequence 23, Appl
128	15	1.1	49272	2	US-08-614-770A-1	Sequence 1, Appli
c 129	14	1.0	21	1	US-08-009-263C-55	Sequence 55, Appl
130	14	1.0	24	1	US-08-411-796-199	Sequence 199, App
131	14	1.0	24	6	PCT-US93-11198-199	Sequence 199, App
c 132	14	1.0	32	1	US-08-530-492-81	Sequence 81, Appl
c 133	14	1.0	36	1	US-08-319-492B-228	Sequence 228, App
c 134	14	1.0	39	2	US-08-481-003-14	Sequence 14, Appl
135	14	1.0	54	1	US-07-982-712-18	Sequence 18, Appl
136	14	1.0	54	1	US-07-875-758-5	Sequence 5, Appli
c 137	14	1.0	60	1	US-08-411-796-62	Sequence 62, Appl
c 138	14	1.0	60	1	US-08-411-796-178	Sequence 178, App
c 139	14	1.0	60	6	PCT-US93-11198-62	Sequence 62, Appl
c 140	14	1.0	60	6	PCT-US93-11198-178	Sequence 178, App
141	14	1.0	64	1	US-08-081-539-15	Sequence 15, Appl
c 142	14	1.0	64	1	US-08-081-539-16	Sequence 16, Appl
143	14	1.0	64	1	US-08-466-647-15	Sequence 15, Appl
c 144	14	1.0	64	1	US-08-466-647-16	Sequence 16, Appl
145	14	1.0	64	1	US-08-411-795B-8	Sequence 8, Appli
c 146	14	1.0	64	1	US-08-411-795B-9	Sequence 9, Appli
147	14	1.0	64	1	US-08-411-795B-142	Sequence 142, App
c 148	14	1.0	64	1	US-08-411-795B-143	Sequence 143, App
149	14	1.0	64	1	US-08-411-796-8	Sequence 8, Appli
c 150	14	1.0	64	1	US-08-411-796-9	Sequence 9, Appli
151	14	1.0	64	2	US-08-469-319A-8	Sequence 8, Appli
c 152	14	1.0	64	2	US-08-469-319A-9	Sequence 9, Appli
153	14	1.0	64	2	US-08-469-319A-142	Sequence 142, App
c 154	14	1.0	64	2	US-08-469-319A-143	Sequence 143, App
155	14	1.0	64	6	PCT-US93-11198-8	Sequence 8, Appli
c 156	14	1.0	64	6	PCT-US93-11198-9	Sequence 9, Appli
157	14	1.0	71	1	US-08-081-539-11	Sequence 11, Appl
c 158	14	1.0	71	1	US-08-081-539-12	Sequence 12, Appl
159	14	1.0	71	1	US-08-466-647-11	Sequence 11, Appl
c 160	14	1.0	71	1	US-08-466-647-12	Sequence 12, Appl
161	14	1.0	71	1	US-08-411-795B-136	Sequence 136, App
c 162	14	1.0	71	1	US-08-411-795B-137	Sequence 137, App
163	14	1.0	71	1	US-08-411-796-136	Sequence 136, App
c 164	14	1.0	71	1	US-08-411-796-137	Sequence 137, App
165	14	1.0	71	2	US-08-469-319A-136	Sequence 136, App
c 166	14	1.0	71	2	US-08-469-319A-137	Sequence 137, App
167	14	1.0	71	6	PCT-US93-11198-136	Sequence 136, App
c 168	14	1.0	71	6	PCT-US93-11198-137	Sequence 137, App
c 169	14	1.0	78	1	US-08-411-796-61	Sequence 61, Appl
c 170	14	1.0	78	1	US-08-411-796-172	Sequence 172, App
c 171	14	1.0	78	1	US-08-411-796-173	Sequence 173, App
c 172	14	1.0	78	1	US-08-411-796-174	Sequence 174, App
c 173	14	1.0	78	1	US-08-411-796-175	Sequence 175, App
c 174	14	1.0	78	1	US-08-411-796-176	Sequence 176, App
c 175	14	1.0	78	1	US-08-411-796-177	Sequence 177, App
c 176	14	1.0	78	6	PCT-US93-11198-61	Sequence 61, Appl
c 177	14	1.0	78	6	PCT-US93-11198-172	Sequence 172, App
c 178	14	1.0	78	6	PCT-US93-11198-173	Sequence 173, App
c 179	14	1.0	78	6	PCT-US93-11198-174	Sequence 174, App
c 180	14	1.0	78	6	PCT-US93-11198-175	Sequence 175, App
c 181	14	1.0	78	6	PCT-US93-11198-176	Sequence 176, App
c 182	14	1.0	78	6	PCT-US93-11198-177	Sequence 177, App
183	14	1.0	146	3	US-08-447-173A-13	Sequence 13, Appl
c 184	14	1.0	159	2	US-08-485-455D-78	Sequence 78, Appl
c 185	14	1.0	159	4	US-08-482-130C-78	Sequence 78, Appl
c 186	14	1.0	159	4	US-08-484-211C-78	Sequence 78, Appl
c 187	14	1.0	159	6	PCT-US95-14442A-78	Sequence 78, Appl
c 188	14	1.0	219	7	5217896-6	Patent No. 5217896
189	14	1.0	240	7	5177308-2	Patent No. 5177308
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191	14	1.0	315	1	US-08-081-539-89	Sequence 89, Appl
192	14	1.0	315	1	US-08-466-647-89	Sequence 89, Appl
193	14	1.0	323	3	US-08-506-864A-4	Sequence 4, Appli
194	14	1.0	323	4	US-08-851-968-4	Sequence 4, Appli
195	14	1.0	330	1	US-08-081-539-84	Sequence 84, Appl
196	14	1.0	330	1	US-08-466-647-84	Sequence 84, Appl
197	14	1.0	333	1	US-08-411-795B-106	Sequence 106, App
198	14	1.0	333	1	US-08-411-795B-107	Sequence 107, App
199	14	1.0	333	1	US-08-411-795B-108	Sequence 108, App
200	14	1.0	333	1	US-08-411-795B-109	Sequence 109, App
201	14	1.0	333	1	US-08-411-795B-110	Sequence 110, App
202	14	1.0	333	1	US-08-411-795B-111	Sequence 111, App
203	14	1.0	333	1	US-08-411-795B-112	Sequence 112, App
204	14	1.0	333	1	US-08-411-795B-113	Sequence 113, App
205	14	1.0	333	1	US-08-411-795B-116	Sequence 116, App
206	14	1.0	333	1	US-08-411-795B-117	Sequence 117, App
207	14	1.0	333	1	US-08-411-795B-118	Sequence 118, App
208	14	1.0	333	2	US-08-469-319A-106	Sequence 106, App
209	14	1.0	333	2	US-08-469-319A-107	Sequence 107, App
210	14	1.0	333	2	US-08-469-319A-108	Sequence 108, App
211	14	1.0	333	2	US-08-469-319A-109	Sequence 109, App
212	14	1.0	333	2	US-08-469-319A-110	Sequence 110, App
213	14	1.0	333	2	US-08-469-319A-111	Sequence 111, App
214	14	1.0	333	2	US-08-469-319A-112	Sequence 112, App
215	14	1.0	333	2	US-08-469-319A-113	Sequence 113, App
216	14	1.0	333	2	US-08-469-319A-116	Sequence 116, App
217	14	1.0	333	2	US-08-469-319A-117	Sequence 117, App
218	14	1.0	333	2	US-08-469-319A-118	Sequence 118, App
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220	14	1.0	336	1	US-08-081-539-79	Sequence 79, Appl
221	14	1.0	336	1	US-08-081-539-80	Sequence 80, Appl
222	14	1.0	336	1	US-08-081-539-81	Sequence 81, Appl
223	14	1.0	336	1	US-08-081-539-82	Sequence 82, Appl
224	14	1.0	336	1	US-08-081-539-83	Sequence 83, Appl
225	14	1.0	336	1	US-08-081-539-85	Sequence 85, Appl
226	14	1.0	336	1	US-08-081-539-86	Sequence 86, Appl
227	14	1.0	336	1	US-08-081-539-87	Sequence 87, Appl
228	14	1.0	336	1	US-08-081-539-88	Sequence 88, Appl
229	14	1.0	336	1	US-08-081-539-90	Sequence 90, Appl
230	14	1.0	336	1	US-08-081-539-91	Sequence 91, Appl
231	14	1.0	336	1	US-08-081-539-96	Sequence 96, Appl
232	14	1.0	336	1	US-08-081-539-97	Sequence 97, Appl
233	14	1.0	336	1	US-08-081-539-100	Sequence 100, App
234	14	1.0	336	1	US-08-081-539-101	Sequence 101, App
235	14	1.0	336	1	US-08-466-647-77	Sequence 77, Appl
236	14	1.0	336	1	US-08-466-647-79	Sequence 79, Appl
237	14	1.0	336	1	US-08-466-647-80	Sequence 80, Appl
238	14	1.0	336	1	US-08-466-647-81	Sequence 81, Appl
239	14	1.0	336	1	US-08-466-647-82	Sequence 82, Appl
240	14	1.0	336	1	US-08-466-647-83	Sequence 83, Appl
241	14	1.0	336	1	US-08-466-647-85	Sequence 85, Appl
242	14	1.0	336	1	US-08-466-647-86	Sequence 86, Appl
243	14	1.0	336	1	US-08-466-647-87	Sequence 87, Appl
244	14	1.0	336	1	US-08-466-647-88	Sequence 88, Appl
245	14	1.0	336	1	US-08-466-647-90	Sequence 90, Appl

	246	14	1.0	336	1	US-08-466-647-91	Sequence 91, Appl
	247	14	1.0	336	1	US-08-466-647-96	Sequence 96, Appl
	248	14	1.0	336	1	US-08-466-647-97	Sequence 97, Appl
	249	14	1.0	336	1	US-08-466-647-100	Sequence 100, App
	250	14	1.0	336	1	US-08-466-647-101	Sequence 101, App
	251	14	1.0	339	1	US-08-081-539-92	Sequence 92, Appl
	252	14	1.0	339	1	US-08-081-539-93	Sequence 93, Appl
	253	14	1.0	339	1	US-08-081-539-102	Sequence 102, App
	254	14	1.0	339	1	US-08-081-539-103	Sequence 103, App
	255	14	1.0	339	1	US-08-466-647-92	Sequence 92, Appl
	256	14	1.0	339	1	US-08-466-647-93	Sequence 93, Appl
	257	14	1.0	339	1	US-08-466-647-102	Sequence 102, App
	258	14	1.0	339	1	US-08-466-647-103	Sequence 103, App
	259	14	1.0	339	1	US-08-411-795B-122	Sequence 122, App
	260	14	1.0	339	1	US-08-411-795B-123	Sequence 123, App
	261	14	1.0	339	1	US-08-411-795B-124	Sequence 124, App
	262	14	1.0	339	1	US-08-411-795B-398	Sequence 398, App
	263	14	1.0	339	1	US-08-411-795B-399	Sequence 399, App
	264	14	1.0	339	1	US-08-411-796-68	Sequence 68, Appl
	265	14	1.0	339	1	US-08-411-796-216	Sequence 216, App
	266	14	1.0	339	1	US-08-411-796-220	Sequence 220, App
	267	14	1.0	339	2	US-08-469-319A-122	Sequence 122, App
	268	14	1.0	339	2	US-08-469-319A-123	Sequence 123, App
	269	14	1.0	339	2	US-08-469-319A-124	Sequence 124, App
	270	14	1.0	339	2	US-08-469-319A-398	Sequence 398, App
	271	14	1.0	339	2	US-08-469-319A-399	Sequence 399, App
	272	14	1.0	339	6	PCT-US93-11198-68	Sequence 68, Appl
	273	14	1.0	339	6	PCT-US93-11198-216	Sequence 216, App
	274	14	1.0	339	6	PCT-US93-11198-220	Sequence 220, App
	275	14	1.0	340	1	US-08-411-795B-408	Sequence 408, App
	276	14	1.0	340	2	US-08-469-319A-408	Sequence 408, App
	277	14	1.0	342	1	US-08-081-539-78	Sequence 78, Appl
	278	14	1.0	342	1	US-08-466-647-78	Sequence 78, Appl
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	280	14	1.0	360	1	US-08-081-539-94	Sequence 94, Appl
	281	14	1.0	360	1	US-08-081-539-99	Sequence 99, Appl
	282	14	1.0	360	1	US-08-466-647-94	Sequence 94, Appl
	283	14	1.0	360	1	US-08-466-647-99	Sequence 99, Appl
	284	14	1.0	378	1	US-08-081-539-95	Sequence 95, Appl
	285	14	1.0	378	1	US-08-466-647-95	Sequence 95, Appl
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	287	14	1.0	408	1	US-08-081-539-104	Sequence 104, App
	288	14	1.0	408	1	US-08-466-647-104	Sequence 104, App
	289	14	1.0	408	1	US-08-411-795B-144	Sequence 144, App
	290	14	1.0	408	1	US-08-411-796-144	Sequence 144, App
	291	14	1.0	408	2	US-08-192-299B-10	Sequence 10, Appl
	292	14	1.0	408	2	US-08-191-973B-10	Sequence 10, Appl
	293	14	1.0	408	2	US-08-469-319A-144	Sequence 144, App
	294	14	1.0	408	3	US-08-470-775-10	Sequence 10, Appl
	295	14	1.0	408	4	US-08-470-509-10	Sequence 10, Appl
	296	14	1.0	408	4	US-08-559-009-10	Sequence 10, Appl
	297	14	1.0	408	6	PCT-US93-11198-144	Sequence 144, App
c	298	14	1.0	414	1	US-08-081-539-120	Sequence 120, App
	299	14	1.0	414	1	US-08-081-539-121	Sequence 121, App
c	300	14	1.0	414	1	US-08-466-647-120	Sequence 120, App
	301	14	1.0	414	1	US-08-466-647-121	Sequence 121, App
	302	14	1.0	414	1	US-08-411-795B-147	Sequence 147, App
c	303	14	1.0	414	1	US-08-411-795B-148	Sequence 148, App
	304	14	1.0	414	1	US-08-411-796-147	Sequence 147, App
c	305	14	1.0	414	1	US-08-411-796-148	Sequence 148, App
	306	14	1.0	414	2	US-08-469-319A-147	Sequence 147, App
c	307	14	1.0	414	2	US-08-469-319A-148	Sequence 148, App
	308	14	1.0	414	6	PCT-US93-11198-147	Sequence 147, App
c	309	14	1.0	414	6	PCT-US93-11198-148	Sequence 148, App
	310	14	1.0	419	2	US-08-486-013-61	Sequence 61, Appl
	311	14	1.0	419	3	US-08-482-279-61	Sequence 61, Appl
	312	14	1.0	419	3	US-08-342-268-61	Sequence 61, Appl
	313	14	1.0	421	2	US-08-486-013-44	Sequence 44, Appl
	314	14	1.0	421	3	US-08-482-279-44	Sequence 44, Appl
	315	14	1.0	421	3	US-08-342-268-44	Sequence 44, Appl
	316	14	1.0	450	4	US-08-387-942C-32	Sequence 32, Appl
	317	14	1.0	456	2	US-08-450-945-70	Sequence 70, Appl
c	318	14	1.0	485	4	US-08-997-080-41	Sequence 41, Appl
c	319	14	1.0	485	4	US-08-997-080-106	Sequence 106, App
c	320	14	1.0	485	4	US-08-997-362-41	Sequence 41, Appl
c	321	14	1.0	485	4	US-08-997-362-106	Sequence 106, App
c	322	14	1.0	485	5	US-08-873-970-41	Sequence 41, Appl
c	323	14	1.0	485	5	US-08-873-970-106	Sequence 106, App
	324	14	1.0	486	3	US-08-858-767-27	Sequence 27, Appl
	325	14	1.0	486	3	US-08-863-028-27	Sequence 27, Appl
c	326	14	1.0	568	4	US-08-505-218-1	Sequence 1, Appli
c	327	14	1.0	568	4	US-08-505-218-12	Sequence 12, Appl
c	328	14	1.0	600	7	5198345-4	Patent No. 5198345
	329	14	1.0	602	1	US-08-229-393-1	Sequence 1, Appli
	330	14	1.0	647	6	PCT-US94-04174-27	Sequence 27, Appl
	331	14	1.0	687	1	US-08-403-388-4	Sequence 4, Appli
	332	14	1.0	687	2	US-08-658-578-4	Sequence 4, Appli
	333	14	1.0	723	3	US-08-618-911-1	Sequence 1, Appli
c	334	14	1.0	729	4	US-08-512-955-3	Sequence 3, Appli
	335	14	1.0	748	2	US-08-471-724-12	Sequence 12, Appl
	336	14	1.0	748	3	US-08-471-969-12	Sequence 12, Appl
	337	14	1.0	748	3	US-08-384-137-12	Sequence 12, Appl
	338	14	1.0	748	4	US-08-470-006A-12	Sequence 12, Appl
	339	14	1.0	748	5	US-08-691-563C-12	Sequence 12, Appl
	340	14	1.0	762	2	US-08-532-390-40	Sequence 40, Appl
	341	14	1.0	783	2	US-08-256-964A-16	Sequence 16, Appl
c	342	14	1.0	807	1	US-08-165-315D-1	Sequence 1, Appli
c	343	14	1.0	824	4	US-08-922-170B-12	Sequence 12, Appl
c	344	14	1.0	846	1	US-08-165-315D-2	Sequence 2, Appli
c	345	14	1.0	850	6	PCT-US95-14442A-102	Sequence 102, App
	346	14	1.0	853	1	US-08-008-216-16	Sequence 16, Appl
	347	14	1.0	853	1	US-08-459-569-16	Sequence 16, Appl
	348	14	1.0	853	2	US-08-458-831-16	Sequence 16, Appl
c	349	14	1.0	858	3	US-08-796-676-2	Sequence 2, Appli
c	350	14	1.0	912	4	US-08-993-228-7	Sequence 7, Appli
c	351	14	1.0	913	1	US-08-109-391A-1	Sequence 1, Appli
c	352	14	1.0	913	1	US-08-459-019A-1	Sequence 1, Appli
c	353	14	1.0	913	4	US-08-460-428A-1	Sequence 1, Appli
	354	14	1.0	925	2	US-08-544-900-3	Sequence 3, Appli
	355	14	1.0	925	6	PCT-US95-07874-2	Sequence 2, Appli
	356	14	1.0	950	7	5177308-3	Patent No. 5177308
c	357	14	1.0	957	1	US-07-745-206A-16	Sequence 16, Appl
c	358	14	1.0	957	3	US-08-311-363-16	Sequence 16, Appl
c	359	14	1.0	972	1	US-08-276-887A-12	Sequence 12, Appl
	360	14	1.0	1029	1	US-08-008-216-15	Sequence 15, Appl
	361	14	1.0	1029	1	US-08-459-569-15	Sequence 15, Appl
	362	14	1.0	1029	2	US-08-458-831-15	Sequence 15, Appl
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	371	14	1.0	1247	2	US-08-643-563A-32	Sequence 32, Appl
	372	14	1.0	1247	2	US-08-643-763A-32	Sequence 32, Appl
	373	14	1.0	1247	2	US-08-462-623-32	Sequence 32, Appl
	374	14	1.0	1247	2	US-08-451-953A-32	Sequence 32, Appl
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	376	14	1.0	1247	4	US-08-461-397A-32	Sequence 32, Appl
	377	14	1.0	1247	4	US-08-912-088-32	Sequence 32, Appl
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	380	14	1.0	1247	6	PCT-US93-08742-32	Sequence 32, Appl
	381	14	1.0	1247	6	PCT-US93-08808-32	Sequence 32, Appl
	382	14	1.0	1247	6	PCT-US93-08885-32	Sequence 32, Appl
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623	14	1.0	4300	6	PCT-US91-09422-1	Sequence 1, Appli
c 624	14	1.0	4344	3	US-08-532-547-4	Sequence 4, Appli
c 625	14	1.0	4344	3	US-08-379-656B-4	Sequence 4, Appli
c 626	14	1.0	4453	2	US-08-770-761A-4	Sequence 4, Appli
c 627	14	1.0	4464	3	US-08-400-159-7	Sequence 7, Appli
c 628	14	1.0	4540	2	US-08-770-761A-6	Sequence 6, Appli
c 629	14	1.0	4594	4	US-08-658-665-43	Sequence 43, Appl
c 630	14	1.0	4594	4	US-08-658-665-45	Sequence 45, Appl
c 631	14	1.0	4621	2	US-08-770-761A-1	Sequence 1, Appli
c 632	14	1.0	4768	4	US-08-658-665-41	Sequence 41, Appl
c 633	14	1.0	4800	6	PCT-US94-07779-1	Sequence 1, Appli
c 634	14	1.0	4909	4	US-08-658-665-68	Sequence 68, Appl
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c 636	14	1.0	4978	1	US-08-220-603A-1	Sequence 1, Appli
c 637	14	1.0	4983	1	US-08-472-358-1	Sequence 1, Appli
c 638	14	1.0	4983	6	PCT-US92-05786A-1	Sequence 1, Appli
c 639	14	1.0	4984	2	US-08-687-806-1	Sequence 1, Appli
c 640	14	1.0	5234	4	US-08-658-665-73	Sequence 73, Appl
641	14	1.0	5236	6	PCT-US91-09422-16	Sequence 16, Appl
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c 643	14	1.0	5399	2	US-08-458-181-9	Sequence 9, Appli
c 644	14	1.0	5399	6	PCT-US93-02172-9	Sequence 9, Appli
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c 662	14	1.0	7175	3	US-08-193-078B-8	Sequence 8, Appli
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c 664	14	1.0	7175	3	US-08-149-097D-8	Sequence 8, Appli
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c 673	14	1.0	8855	3	US-08-322-760A-1	Sequence 1, Appli
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676	14	1.0	9401	1	US-07-910-760-9	Sequence 9, Appli
677	14	1.0	9401	2	US-08-440-519-9	Sequence 9, Appli
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679	14	1.0	9401	6	PCT-US91-02225-9	Sequence 9, Appli
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c 685	14	1.0	11663	5	US-09-102-248-7	Sequence 7, Appli
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c 687	14	1.0	11703	5	US-09-102-248-8	Sequence 8, Appli
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696	14	1.0	12616	4	US-08-822-445-9	Sequence 9, Appli
697	14	1.0	12847	2	US-08-550-715-1	Sequence 1, Appli
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699	14	1.0	13254	1	US-08-276-852-170	Sequence 170, App
c 700	14	1.0	13254	2	US-08-899-575-156	Sequence 156, App
701	14	1.0	13254	2	US-08-899-575-170	Sequence 170, App
c 702	14	1.0	13254	2	US-08-899-575-156	Sequence 156, App
703	14	1.0	13254	2	US-08-899-575-170	Sequence 170, App
c 704	14	1.0	13254	6	PCT-US95-08743-156	Sequence 156, App
705	14	1.0	13254	6	PCT-US95-08743-170	Sequence 170, App
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c 709	14	1.0	16656	2	US-08-739-158-1	Sequence 1, Appli
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711	14	1.0	18318	2	US-08-414-926A-6	Sequence 6, Appli
712	14	1.0	18318	4	US-08-926-922-6	Sequence 6, Appli
713	14	1.0	18912	6	PCT-US96-03916-59	Sequence 59, Appl
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717	14	1.0	21126	1	US-08-459-569-19	Sequence 19, Appl
718	14	1.0	21126	2	US-08-458-831-19	Sequence 19, Appl
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723	14	1.0	246240	3	US-08-724-394A-20	Sequence 20, Appl
724	14	1.0	246240	3	US-08-724-394A-21	Sequence 21, Appl
725	14	1.0	246240	3	US-08-724-394A-22	Sequence 22, Appl
726	13	0.9	14	6	PCT-US96-09383-15	Sequence 15, Appl
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728	13	0.9	19	1	US-08-031-143B-58	Sequence 58, Appl
729	13	0.9	19	6	PCT-US94-02891-58	Sequence 58, Appl
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731	13	0.9	20	5	US-09-102-248-11	Sequence 11, Appl
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734	13	0.9	26	3	US-08-482-182-21	Sequence 21, Appl
735	13	0.9	26	3	US-08-482-182-64	Sequence 64, Appl
736	13	0.9	26	4	US-08-766-439-48	Sequence 48, Appl
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738	13	0.9	29	1	US-08-530-492-14	Sequence 14, Appl
739	13	0.9	29	2	US-08-464-531-35	Sequence 35, Appl
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c 742	13	0.9	30	1	US-07-855-417A-27	Sequence 27, Appl
743	13	0.9	31	4	US-08-415-593-18	Sequence 18, Appl
744	13	0.9	32	1	US-07-951-715A-43	Sequence 43, Appl
745	13	0.9	32	3	US-08-459-448A-43	Sequence 43, Appl
746	13	0.9	33	1	US-08-331-398A-29	Sequence 29, Appl
c 747	13	0.9	33	1	US-08-434-503-51	Sequence 51, Appl
748	13	0.9	33	1	US-08-225-224-46	Sequence 46, Appl
749	13	0.9	33	4	US-08-331-397B-29	Sequence 29, Appl
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751	13	0.9	33	5	US-08-722-258-46	Sequence 46, Appl
752	13	0.9	33	6	PCT-US95-04468-46	Sequence 46, Appl
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754	13	0.9	36	1	US-08-423-399B-25	Sequence 25, Appl
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c 756	13	0.9	36	2	US-08-334-847-742	Sequence 742, App
c 757	13	0.9	36	3	US-08-585-684B-2033	Sequence 2033, Ap
c 758	13	0.9	36	3	US-08-585-684B-2034	Sequence 2034, Ap
c 759	13	0.9	36	3	US-08-585-684B-2035	Sequence 2035, Ap
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761	13	0.9	39	2	US-08-338-992B-4	Sequence 4, Appli
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763	13	0.9	39	3	US-08-750-810-4	Sequence 4, Appli
c 764	13	0.9	39	6	PCT-US95-09057-3	Sequence 3, Appli
765	13	0.9	39	6	PCT-US95-09057-4	Sequence 4, Appli
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769	13	0.9	54	3	US-08-622-956-1	Sequence 1, Appli
770	13	0.9	54	4	US-08-923-274-5	Sequence 5, Appli
771	13	0.9	54	4	US-08-959-536-5	Sequence 5, Appli
c 772	13	0.9	59	1	US-07-972-032-26	Sequence 26, Appl
773	13	0.9	59	1	US-07-972-032-27	Sequence 27, Appl
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775	13	0.9	59	2	US-08-642-255-41	Sequence 41, Appl
776	13	0.9	60	1	US-08-247-475-9	Sequence 9, Appli
777	13	0.9	60	1	US-08-479-650-9	Sequence 9, Appli
778	13	0.9	60	1	US-08-278-630A-1	Sequence 1, Appli
779	13	0.9	60	1	US-08-331-394-57	Sequence 57, Appl
780	13	0.9	60	2	US-08-250-858-57	Sequence 57, Appl
781	13	0.9	60	2	US-08-446-915-57	Sequence 57, Appl
782	13	0.9	60	2	US-08-191-866D-10	Sequence 10, Appl
783	13	0.9	60	2	US-08-674-169-9	Sequence 9, Appli
784	13	0.9	60	3	US-08-744-139-55	Sequence 55, Appl
785	13	0.9	60	3	US-08-185-949B-10	Sequence 10, Appl
786	13	0.9	60	6	PCT-US95-06639-57	Sequence 57, Appl
787	13	0.9	66	2	US-08-323-531-23	Sequence 23, Appl
788	13	0.9	66	2	US-08-198-094-23	Sequence 23, Appl
c 789	13	0.9	66	2	US-08-606-789-28	Sequence 28, Appl
c 790	13	0.9	66	4	US-09-111-348-28	Sequence 28, Appl
791	13	0.9	66	6	PCT-US93-07424-23	Sequence 23, Appl
792	13	0.9	66	6	PCT-US95-02087-23	Sequence 23, Appl
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794	13	0.9	73	1	US-08-260-515-10	Sequence 10, Appl
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796	13	0.9	74	1	US-08-260-515-12	Sequence 12, Appl
797	13	0.9	74	1	US-08-260-515-16	Sequence 16, Appl
798	13	0.9	74	1	US-08-260-515-19	Sequence 19, Appl
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c 801	13	0.9	77	4	US-08-477-527A-241	Sequence 241, App
c 802	13	0.9	77	6	PCT-US96-09537-241	Sequence 241, App
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804	13	0.9	85	1	US-08-479-725-30	Sequence 30, Appl
805	13	0.9	85	2	US-08-618-693-30	Sequence 30, Appl
806	13	0.9	85	6	PCT-US96-08014-119	Sequence 119, App
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c 808	13	0.9	106	1	US-08-413-118-110	Sequence 110, App
c 809	13	0.9	108	1	US-07-972-032-30	Sequence 30, Appl
c 810	13	0.9	108	2	US-08-642-255-44	Sequence 44, Appl
811	13	0.9	112	1	US-08-413-118-109	Sequence 109, App
c 812	13	0.9	121	1	US-07-977-630-84	Sequence 84, Appl
c 813	13	0.9	126	1	US-08-248-848-37	Sequence 37, Appl
c 814	13	0.9	126	2	US-08-111-077-37	Sequence 37, Appl
c 815	13	0.9	135	1	US-08-161-406-3	Sequence 3, Appli
c 816	13	0.9	162	1	US-07-972-032-34	Sequence 34, Appl
c 817	13	0.9	162	1	US-07-972-032-36	Sequence 36, Appl
818	13	0.9	163	7	5486462-4	Patent No. 5486462
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c 820	13	0.9	194	4	US-09-111-348-11	Sequence 11, Appl
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822	13	0.9	199	6	PCT-US92-10087-4	Sequence 4, Appli
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c 824	13	0.9	216	1	US-08-031-143B-75	Sequence 75, Appl
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827	13	0.9	219	1	US-08-264-526-3	Sequence 3, Appli
828	13	0.9	240	2	US-08-485-455D-58	Sequence 58, Appl
829	13	0.9	240	4	US-08-482-130C-58	Sequence 58, Appl

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	831	13	0.9	240	6	PCT-US95-14442A-58	Sequence 58, Appl
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	833	13	0.9	263	2	US-08-594-031-108	Sequence 108, App
	834	13	0.9	265	2	US-08-709-616-2	Sequence 2, Appli
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c	836	13	0.9	276	1	US-08-057-168-1	Sequence 1, Appli
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	838	13	0.9	277	2	US-08-518-878B-19	Sequence 19, Appl
	839	13	0.9	277	2	US-08-294-522B-18	Sequence 18, Appl
	840	13	0.9	277	2	US-08-294-522B-19	Sequence 19, Appl
	841	13	0.9	277	3	US-08-807-861A-18	Sequence 18, Appl
	842	13	0.9	277	3	US-08-807-861A-19	Sequence 19, Appl
	843	13	0.9	277	3	US-08-470-868A-18	Sequence 18, Appl
	844	13	0.9	277	3	US-08-470-868A-19	Sequence 19, Appl
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c	846	13	0.9	292	4	US-09-111-348-14	Sequence 14, Appl
	847	13	0.9	302	1	US-08-189-199A-1	Sequence 1, Appli
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	849	13	0.9	312	1	US-08-008-216-5	Sequence 5, Appli
	850	13	0.9	312	1	US-08-459-569-5	Sequence 5, Appli
	851	13	0.9	312	2	US-08-458-831-5	Sequence 5, Appli
	852	13	0.9	331	3	US-07-916-098A-22	Sequence 22, Appl
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c	854	13	0.9	354	3	US-08-652-816A-23	Sequence 23, Appl
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	857	13	0.9	365	3	US-07-916-098A-8	Sequence 8, Appli
	858	13	0.9	366	3	US-07-916-098A-9	Sequence 9, Appli
c	859	13	0.9	367	3	US-08-967-101-24	Sequence 24, Appl
c	860	13	0.9	367	4	US-08-592-541-24	Sequence 24, Appl
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c	862	13	0.9	390	5	US-08-803-085-1	Sequence 1, Appli
	863	13	0.9	392	1	US-08-318-193-1	Sequence 1, Appli
	864	13	0.9	393	1	US-07-846-992-10	Sequence 10, Appl
	865	13	0.9	393	1	US-08-469-555-10	Sequence 10, Appl
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c	867	13	0.9	394	2	US-08-467-282B-103	Sequence 103, App
c	868	13	0.9	394	3	US-08-471-282A-103	Sequence 103, App
c	869	13	0.9	394	3	US-08-466-710C-103	Sequence 103, App
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	871	13	0.9	406	1	US-08-318-193-52	Sequence 52, Appl
	872	13	0.9	414	4	US-09-067-773-2	Sequence 2, Appli
	873	13	0.9	414	4	US-09-067-773-6	Sequence 6, Appli
	874	13	0.9	414	4	US-09-067-773-9	Sequence 9, Appli
c	875	13	0.9	420	3	US-08-736-334B-3	Sequence 3, Appli
c	876	13	0.9	422	1	US-07-920-519-33	Sequence 33, Appl
c	877	13	0.9	422	1	US-08-314-586-33	Sequence 33, Appl
	878	13	0.9	422	1	US-08-470-179-73	Sequence 73, Appl
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c	880	13	0.9	422	5	US-07-927-391-14	Sequence 14, Appl
c	881	13	0.9	423	1	US-08-470-179-67	Sequence 67, Appl
	882	13	0.9	423	1	US-08-470-179-72	Sequence 72, Appl
	883	13	0.9	423	1	US-08-470-179-81	Sequence 81, Appl
	884	13	0.9	423	1	US-08-470-179-83	Sequence 83, Appl
c	885	13	0.9	423	1	US-08-470-179-85	Sequence 85, Appl
c	886	13	0.9	423	1	US-08-470-179-96	Sequence 96, Appl
	887	13	0.9	423	1	US-08-470-179-130	Sequence 130, App
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	889	13	0.9	423	1	US-08-470-179-169	Sequence 169, App
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	892	13	0.9	423	1	US-08-470-179-194	Sequence 194, App
c	893	13	0.9	432	2	US-08-642-255-48	Sequence 48, Appl
	894	13	0.9	447	4	US-08-387-942C-33	Sequence 33, Appl
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	896	13	0.9	450	1	US-08-399-580B-2	Sequence 2, Appli
	897	13	0.9	453	2	US-08-470-892-4	Sequence 4, Appli
c	898	13	0.9	454	4	US-08-680-326-118	Sequence 118, App
	899	13	0.9	461	3	US-07-916-098A-38	Sequence 38, Appl
	900	13	0.9	487	1	US-08-485-359-3	Sequence 3, Appli
	901	13	0.9	487	1	US-08-569-594-3	Sequence 3, Appli
	902	13	0.9	487	6	PCT-US96-08815-3	Sequence 3, Appli
c	903	13	0.9	489	1	US-08-081-072-9	Sequence 9, Appli
c	904	13	0.9	489	1	US-08-449-093A-9	Sequence 9, Appli
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	906	13	0.9	498	1	US-08-412-614-90	Sequence 90, Appl
	907	13	0.9	498	4	US-08-635-761-90	Sequence 90, Appl
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c	912	13	0.9	518	4	US-08-557-309B-1	Sequence 1, Appli
	913	13	0.9	519	4	US-08-799-464A-23	Sequence 23, Appl
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	918	13	0.9	525	1	US-08-569-594-1	Sequence 1, Appli
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	923	13	0.9	525	6	PCT-US94-12873-1	Sequence 1, Appli
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c	926	13	0.9	537	1	US-08-176-620A-9	Sequence 9, Appli
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	928	13	0.9	537	6	PCT-US94-12873-16	Sequence 16, Appl
	929	13	0.9	541	3	US-08-797-689-13	Sequence 13, Appl
	930	13	0.9	545	2	US-08-599-252-86	Sequence 86, Appl
c	931	13	0.9	545	6	PCT-US95-06406A-22	Sequence 22, Appl
	932	13	0.9	545	6	PCT-US96-06352-86	Sequence 86, Appl
	933	13	0.9	545	6	PCT-US96-06583-86	Sequence 86, Appl
	934	13	0.9	546	6	PCT-US95-01185-177	Sequence 177, App
	935	13	0.9	546	6	PCT-US95-01185-178	Sequence 178, App
	936	13	0.9	546	6	PCT-US95-01185-179	Sequence 179, App
	937	13	0.9	549	1	US-08-412-614-92	Sequence 92, Appl
	938	13	0.9	549	4	US-08-635-761-92	Sequence 92, Appl
	939	13	0.9	555	6	PCT-US94-12873-13	Sequence 13, Appl
c	940	13	0.9	560	3	US-08-484-993B-44	Sequence 44, Appl
c	941	13	0.9	560	4	US-08-484-158B-44	Sequence 44, Appl
c	942	13	0.9	560	4	US-08-484-596A-44	Sequence 44, Appl
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	946	13	0.9	563	2	US-08-463-115-32	Sequence 32, Appl
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	948	13	0.9	574	2	US-08-765-081-2	Sequence 2, Appli
	949	13	0.9	574	6	PCT-US95-06994-2	Sequence 2, Appli
c	950	13	0.9	581	3	US-08-505-617-5	Sequence 5, Appli
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	954	13	0.9	586	2	US-07-869-933-26	Sequence 26, Appl
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c	957	13	0.9	595	6	PCT-US94-02034-1	Sequence 1, Appli
c	958	13	0.9	596	3	US-08-676-279-63	Sequence 63, Appl
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	970	13	0.9	636	4	US-08-447-642-3	Sequence 3, Appli
	971	13	0.9	636	6	PCT-US93-02147A-3	Sequence 3, Appli
	972	13	0.9	641	1	US-07-846-992-9	Sequence 9, Appli
	973	13	0.9	641	1	US-08-469-555-9	Sequence 9, Appli
	974	13	0.9	642	1	US-08-287-442-1	Sequence 1, Appli
	975	13	0.9	642	1	US-08-287-442-5	Sequence 5, Appli

976	13	0.9	642	1	US-08-459-701-1	Sequence 1, Appli
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978	13	0.9	642	1	US-08-460-298-1	Sequence 1, Appli
979	13	0.9	642	1	US-08-460-298-5	Sequence 5, Appli
980	13	0.9	642	2	US-08-459-174-1	Sequence 1, Appli
981	13	0.9	642	2	US-08-459-174-5	Sequence 5, Appli
982	13	0.9	642	2	US-08-761-258-2	Sequence 2, Appli
983	13	0.9	642	2	US-08-761-258-4	Sequence 4, Appli
984	13	0.9	642	2	US-08-761-258-9	Sequence 9, Appli
985	13	0.9	642	3	US-09-009-218-1	Sequence 1, Appli
986	13	0.9	642	3	US-09-009-218-3	Sequence 3, Appli
987	13	0.9	642	3	US-09-009-218-5	Sequence 5, Appli
988	13	0.9	642	3	US-09-009-218-7	Sequence 7, Appli
989	13	0.9	642	3	US-09-009-218-9	Sequence 9, Appli
990	13	0.9	642	4	US-08-977-306-2	Sequence 2, Appli
991	13	0.9	642	4	US-08-977-306-4	Sequence 4, Appli
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994	13	0.9	642	6	PCT-US93-06300A-5	Sequence 5, Appli
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c 997	13	0.9	664	3	US-08-835-099A-15	Sequence 15, Appl
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ALIGNMENTS

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RESULT   1
US-08-764-233A-1/c
; Sequence 1, Application US/08764233A
; Patent No. 5716849
;  GENERAL INFORMATION:
;    APPLICANT:  Ligon, James M.
;    APPLICANT:  Schupp, Thomas
;    APPLICANT:  Beck, James J.
;    APPLICANT:  Hill, Dwight S.
;    APPLICANT:  Neff, Snezanna
;    APPLICANT:  Ryals, John A.
;    TITLE OF INVENTION:  Genes For The Biosynthesis Of Soraphen
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ciba-Geigy Corporation
;      STREET:  520 White Plains Road, P.O. Box 2005
;      CITY:  Tarrytown
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10591
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/764,233A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/729,214
;      FILING DATE:  09-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/258,261
;      FILING DATE:  08-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meigs, J. Timothy
;      REGISTRATION NUMBER:  38,241
;      REFERENCE/DOCKET NUMBER:  1506/CIP6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 541-8587
;      TELEFAX:  (919) 541-8689
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  49377 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  Sorangium cellulosum
;    IMMEDIATE SOURCE:
;      CLONE:  p98/1, pJL3, and pVKM15
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;      LOCATION:  383..760
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;      OTHER INFORMATION:  /note= "This gene encodes a protein that is highly homolog
;      OTHER INFORMATION:  the reductase domains of type I PKSs such as eryA from
;      OTHER INFORMATION:  Saccharopolyspora erythraea."
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  927..19874
;      OTHER INFORMATION:  /product= "SorA"
;      OTHER INFORMATION:  /note= "Gene product is highly homologous to type I PKS t
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;      OTHER INFORMATION:  compounds."
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;      NAME/KEY:  misc_feature
;      LOCATION:  942..7115
;      OTHER INFORMATION:  /product= "Module 1 of SorA"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  7203..12884
;      OTHER INFORMATION:  /product= "Module 2 of SorA"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  13455..19616
;      OTHER INFORMATION:  /product= "Module 3 of SorA"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  19871..46318
;      OTHER INFORMATION:  /product= "SorB"
;      OTHER INFORMATION:  /note= "Gene product is highly homologous to type I PKS ge
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;      NAME/KEY:  misc_feature
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;      OTHER INFORMATION:  /product= "Module 1 of SorB"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  24638..30820
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;    FEATURE:
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;      LOCATION:  30881..35446
;      OTHER INFORMATION:  /product= "Module 3 of SorB"
;    FEATURE:
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;      LOCATION:  35528..40114
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;      LOCATION:  40190..46318
;      OTHER INFORMATION:  /product= "Module 5 of SorB"
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;      NAME/KEY:  misc_feature
;      LOCATION:  46851..47891
;      OTHER INFORMATION:  /product= "SorM"
;      OTHER INFORMATION:  /note= "The protein encoded by the sorM gene is highly
;      OTHER INFORMATION:  homologous to the methyltransferase from Streptomyces
;      OTHER INFORMATION:  hygroscopicus that is involved in the synthesis of the
;      OTHER INFORMATION:  polyketide rappamicin."
US-08-764-233A-1

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Db  49054 ACGGCTACATCCTGACC 49038


RESULT   2
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; Sequence 27, Application PC/TUS9102942
;  GENERAL INFORMATION:
;    APPLICANT:  ROTHLEIN, ROBERT
;    APPLICANT:  ADAIR, JOHN R
;    APPLICANT:  ATHWAL, DILJEET S
;    TITLE OF INVENTION:  HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
;    NUMBER OF SEQUENCES:  102
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1225 Connecticut Ave. NW Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/02942
;      FILING DATE:  19910429
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9009549.8
;      FILING DATE:  27-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FOX, SAM L
;      REGISTRATION NUMBER:  30,353
;      REFERENCE/DOCKET NUMBER:  1011.0586600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 466-0800
;      TELEFAX:  (202) 833-8716
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  76 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US91-02942-27


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RESULT   3
US-08-171-385-10/c
; Sequence 10, Application US/08171385
; Patent No. 5527884
;  GENERAL INFORMATION:
;    APPLICANT:  Mary E. Russell
;    APPLICANT:  Ulrike Utans
;    TITLE OF INVENTION:  Mediators of Chronic Allograft
;    TITLE OF INVENTION:  Rejection
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  MS-DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/171,385
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fraser, Janis K.
;      REGISTRATION NUMBER:  34,819
;      REFERENCE/DOCKET NUMBER:  05433/006001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  388
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-171-385-10


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RESULT   4
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; Sequence 4, Application US/08534910B
; Patent No. 5766911
;  GENERAL INFORMATION:
;    APPLICANT:  KOIKE, Ayumi
;    APPLICANT:  OBATA, Shusei
;    APPLICANT:  NISHINO, Tokuzo
;    APPLICANT:  OHNUMA, Shinichi
;    APPLICANT:  NAKAZAWA, Takeshi
;    APPLICANT:  OGURA, Kyozo
;    APPLICANT:  KOYAMA, Tanetoshi
;    TITLE OF INVENTION:  Mutated Farnesyldiphosphate Synthase Capable
;    TITLE OF INVENTION:  Of Synthesizing Geranylgeranyldiphosphate And Gene Coding T
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenyon & Kenyon
;      STREET:  1025 Connecticut Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  U.S.
;      ZIP:  20036-5405
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.25" Floppy Disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS 6.2
;      SOFTWARE:  IBM/Word Perfect 6.1 Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/534,910B
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;      FILING DATE:  28-SEPT-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-25253
;      FILING DATE:  14-FEB-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Toffenetti, Judith L.
;      REGISTRATION NUMBER:  39,048
;      REFERENCE/DOCKET NUMBER:  77670/398
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)429-1776
;      TELEFAX:  (202)429-0796
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  894 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Bacillus stearothermophilus
US-08-534-910B-4


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RESULT   5
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; Sequence 4, Application US/08860368B
; Patent No. 6002072
;  GENERAL INFORMATION:
;    APPLICANT:  McMaster, Russell J.
;    APPLICANT:  Boeshore, Maury L.
;    APPLICANT:  Tricoli, David M.
;    APPLICANT:  Reynolds, John F.
;    APPLICANT:  Carney, Kim J.
;    APPLICANT:  Gonsalves, Dennis
;    TITLE OF INVENTION:  Papaya Ringspot Virus Coat Protein Gene
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rockey, Milnamow & Katz, Ltd.
;      STREET:  180 N. Stetson Avenue, 2 Prudential Plaza,
;      STREET:  Suite 4700
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  U.S.A.
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,368B
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueller, Lisa L.
;      REGISTRATION NUMBER:  38,978
;      REFERENCE/DOCKET NUMBER:  SVS3801P0181US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5400
;      TELEFAX:  312-616-5460
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  929 base pairs
;      TYPE:  nucleic acid
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;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA (genomic)
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US-08-860-368B-4


  Query Match             1.1%;  Score 16;  DB 5;  Length 929;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    139 gacggcagtgtcagta 154
          ||||||||||||||||
Db    780 GACGGCAGTGTCAGTA 795


RESULT   6
US-08-860-368B-19
; Sequence 19, Application US/08860368B
; Patent No. 6002072
;  GENERAL INFORMATION:
;    APPLICANT:  McMaster, Russell J.
;    APPLICANT:  Boeshore, Maury L.
;    APPLICANT:  Tricoli, David M.
;    APPLICANT:  Reynolds, John F.
;    APPLICANT:  Carney, Kim J.
;    APPLICANT:  Gonsalves, Dennis
;    TITLE OF INVENTION:  Papaya Ringspot Virus Coat Protein Gene
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rockey, Milnamow & Katz, Ltd.
;      STREET:  180 N. Stetson Avenue, 2 Prudential Plaza,
;      STREET:  Suite 4700
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  U.S.A.
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,368B
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueller, Lisa L.
;      REGISTRATION NUMBER:  38,978
;      REFERENCE/DOCKET NUMBER:  SVS3801P0181US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5400
;      TELEFAX:  312-616-5460
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1155 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA (genomic)
US-08-860-368B-19


  Query Match             1.1%;  Score 16;  DB 5;  Length 1155;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy    139 gacggcagtgtcagta 154
          ||||||||||||||||
Db   1006 GACGGCAGTGTCAGTA 1021


RESULT   7
US-08-860-368B-1
; Sequence 1, Application US/08860368B
; Patent No. 6002072
;  GENERAL INFORMATION:
;    APPLICANT:  McMaster, Russell J.
;    APPLICANT:  Boeshore, Maury L.
;    APPLICANT:  Tricoli, David M.
;    APPLICANT:  Reynolds, John F.
;    APPLICANT:  Carney, Kim J.
;    APPLICANT:  Gonsalves, Dennis
;    TITLE OF INVENTION:  Papaya Ringspot Virus Coat Protein Gene
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rockey, Milnamow & Katz, Ltd.
;      STREET:  180 N. Stetson Avenue, 2 Prudential Plaza,
;      STREET:  Suite 4700
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  U.S.A.
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,368B
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueller, Lisa L.
;      REGISTRATION NUMBER:  38,978
;      REFERENCE/DOCKET NUMBER:  SVS3801P0181US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5400
;      TELEFAX:  312-616-5460
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1158 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1102
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1105..1158
US-08-860-368B-1


  Query Match             1.1%;  Score 16;  DB 5;  Length 1158;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    139 gacggcagtgtcagta 154
          ||||||||||||||||
Db   1009 GACGGCAGTGTCAGTA 1024


RESULT   8
US-08-142-897-4
; Sequence 4, Application US/08142897
; Patent No. 5447852
;  GENERAL INFORMATION:
;    APPLICANT:  Friedman, Jeffrey S.
;    APPLICANT:  Weissman, Irving L.
;    TITLE OF INVENTION:  No. 5447852el Cyclophilins, Associating Proteins
;    TITLE OF INVENTION:  and Uses
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Tracy J. Dunn
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,897
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/005,917
;      FILING DATE:  15-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/740,375
;      FILING DATE:  05-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dunn, Tracy D.
;      REGISTRATION NUMBER:  34,587
;      REFERENCE/DOCKET NUMBER:  5490A-92-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1288 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  53..691
US-08-142-897-4


  Query Match             1.1%;  Score 16;  DB 1;  Length 1288;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    448 atcaaagtcctgctca 463
          ||||||||||||||||
Db    982 ATCAAAGTCCTGCTCA 997


RESULT   9
US-08-476-008-68/c
; Sequence 68, Application US/08476008
; Patent No. 5627061
;  GENERAL INFORMATION:
;    APPLICANT:  Barry, Gerard F.
;    APPLICANT:  Kishore, Ganesh M.
;    APPLICANT:  Padgette, Stephen R.
;    APPLICANT:  Stallings, William C.
;    TITLE OF INVENTION:  Glyphosate Tolerant
;    TITLE OF INVENTION:  5-Enolpyruvylshikimate-3-Phosphate Synthases
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis R. Hoerner, Jr., Monsanto Co. BB4F
;      STREET:  700 Chesterfield Village Parkway
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
```

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;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/476,008
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/306,063
;      FILING DATE:  13-SEP-1994
;      APPLICATION NUMBER:  US 07/749,611
;      FILING DATE:  28-AUG-1991
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/576,537
;      FILING DATE:  31-AUG-1990
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hoerner Jr., Dennis R.
;      REGISTRATION NUMBER:  30,914
;      REFERENCE/DOCKET NUMBER:  38-21(10660)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6099
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1479 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  107..1438
US-08-476-008-68


  Query Match             1.1%;  Score 16;  DB 1;  Length 1479;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    481 accgccaaactcatcg 496
          ||||||||||||||||
Db   1299 ACCGCCAAACTCATCG 1284


RESULT  10
US-08-306-063-68/c
; Sequence 68, Application US/08306063
; Patent No. 5633435
;  GENERAL INFORMATION:
;    APPLICANT:  Barry, Gerard F.
;    APPLICANT:  Kishore, Ganesh M.
;    APPLICANT:  Padgette, Stephen R.
;    APPLICANT:  Stallings, William C.
;    TITLE OF INVENTION:  Glyphosate Tolerant
;    TITLE OF INVENTION:  5-Enolpyruvylshikimate-3-Phosphate Synthases
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis R. Hoerner, Jr., Monsanto Co. BB4F
;      STREET:  700 Chesterfield Village Parkway
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/306,063
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/749,611
;      FILING DATE:  28-AUG-1991
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/576,537
;      FILING DATE:  31-AUG-1990
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hoerner Jr., Dennis R.
;      REGISTRATION NUMBER:  30,914
;      REFERENCE/DOCKET NUMBER:  38-21(10660)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6099
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1479 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  107..1438
US-08-306-063-68


  Query Match             1.1%;  Score 16;  DB 1;  Length 1479;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    481 accgccaaactcatcg 496
          ||||||||||||||||
Db   1299 ACCGCCAAACTCATCG 1284


RESULT  11
US-08-833-485-68/c
; Sequence 68, Application US/08833485
; Patent No. 5804425
;  GENERAL INFORMATION:
;    APPLICANT:  Barry, Gerard F.
;    APPLICANT:  Kishore, Ganesh M.
;    APPLICANT:  Padgette, Stephen R.
;    APPLICANT:  Stallings, William C.
;    TITLE OF INVENTION:  Glyphosate Tolerant
;    TITLE OF INVENTION:  5-Enolpyruvylshikimate-3-Phosphate Synthases
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis R. Hoerner, Jr., Monsanto Co. BB4F
;      STREET:  700 Chesterfield Village Parkway
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/833,485
;      FILING DATE:  07-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/306,063
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:  435
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/749,611
;      FILING DATE:  28-AUG-1991
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/576,537
;      FILING DATE:  31-AUG-1990
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hoerner Jr., Dennis R.
;      REGISTRATION NUMBER:  30,914
;      REFERENCE/DOCKET NUMBER:  38-21(15117)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)737-6099
;      TELEFAX:  (314)737-6047
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1479 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  107..1438
US-08-833-485-68


  Query Match              1.1%;  Score 16;  DB 2;  Length 1479;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     481 accgccaaactcatcg 496
           ||||||||||||||||
Db    1299 ACCGCCAAACTCATCG 1284


RESULT  12
US-08-204-656B-9
; Sequence 9, Application US/08204656B
; Patent No. 5538882
;  GENERAL INFORMATION:
;    APPLICANT:  Matsui, Ikuo
;    APPLICANT:  Ishikawa, Kazuhiko
;    APPLICANT:  Miyairi, Sachio
;    APPLICANT:  Honda, Koichi
;    TITLE OF INVENTION:  Variant-Type Carbohydrate Hydrolase,
;    TITLE OF INVENTION:  Variant Gene Of The Enzyme And Method For Producing
;    TITLE OF INVENTION:  Oligosaccharide Using The Enzyme
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Birch, Stewart, Kolasch & Birch, LLP
;      STREET:  8110 Gatehouse Road, Suite 500 East
;      CITY:  Falls Church
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22042
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,656B
;      FILING DATE:  02-MAR-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weiner, Marc S.
;      REGISTRATION NUMBER:  32,181
;      REFERENCE/DOCKET NUMBER:  234-252P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
;      TELEX:  248345
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2061 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Synthetic DNA"
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      LIBRARY:  Library of chromosomal DNA from Bacillus
;      LIBRARY:  macerans, pMAC, generated by treating chromosomal DNA from Bacillus
;      LIBRARY:  IAM1243 with a restriction enzyme, and inserting and linking restric
;      LIBRARY:  fragments to pBR322
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2061
;      OTHER INFORMATION:  /note= "Nucleotides 1-2061
;      OTHER INFORMATION:  correspond to nucleotides 82-2142 of the Bacillus macerans
;      OTHER INFORMATION:  cyclomaltodextrin glucanotransferase structural gene"
US-08-204-656B-9


  Query Match              1.1%;  Score 16;  DB 1;  Length 2061;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1171 ggcaacgccgccgagc 1186
           ||||||||||||||||
Db    1825 GGCAACGCCGCCGAGC 1840


RESULT  13
US-08-470-702-5
; Sequence 5, Application US/08470702
; Patent No. 5631149
;  GENERAL INFORMATION:
;    APPLICANT:  MATSUI, IKUO
;    APPLICANT:  ISHIKAWA, KAZUHIKO
;    APPLICANT:  MIYAIRI, SACHIO
;    APPLICANT:  HONDA, KOICHI
;    TITLE OF INVENTION:  VARIANT-TYPE CARBOHYDRATE HYDROLASE,
;    TITLE OF INVENTION:  VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
;    TITLE OF INVENTION:  OLIGOSACCHARIDE USING THE ENZYME
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH & BIRCH
;      STREET:  8110 Gatehouse Road, Suite 500 East
;      CITY:  Falls Church
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22042
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,702
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/204,656
;      FILING DATE:  02-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEINER, MARC S.
;      REGISTRATION NUMBER:  32,181
;      REFERENCE/DOCKET NUMBER:  234-252P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
```

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;      TELEX:  248345
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2061 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (synthetic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-470-702-5


  Query Match             1.1%;  Score 16;  DB 1;  Length 2061;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1171 ggcaacgccgccgagc 1186
          ||||||||||||||||
Db   1825 GGCAACGCCGCCGAGC 1840


RESULT  14
US-08-467-831-5
; Sequence 5, Application US/08467831
; Patent No. 5635378
;  GENERAL INFORMATION:
;    APPLICANT:  MATSUI, IKUO
;    APPLICANT:  ISHIKAWA, KAZUHIKO
;    APPLICANT:  MIYAIRI, SACHIO
;    APPLICANT:  HONDA, KOICHI
;    TITLE OF INVENTION:  VARIANT-TYPE CARBOHYDRATE HYDROLASE,
;    TITLE OF INVENTION:  VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
;    TITLE OF INVENTION:  OLIGOSACCHARIDE USING THE ENZYME
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH & BIRCH
;      STREET:  8110 Gatehouse Road, Suite 500 East
;      CITY:  Falls Church
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22042
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,831
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/204,656
;      FILING DATE:  02-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEINER, MARC S.
;      REGISTRATION NUMBER:  32,181
;      REFERENCE/DOCKET NUMBER:  234-252P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
;      TELEX:  248345
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2061 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (synthetic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-467-831-5


  Query Match             1.1%;  Score 16;  DB 1;  Length 2061;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1171 ggcaacgccgccgagc 1186
          ||||||||||||||||
Db   1825 GGCAACGCCGCCGAGC 1840


RESULT  15
US-08-132-990A-7
; Sequence 7, Application US/08132990A
; Patent No. 5834589
;  GENERAL INFORMATION:
;    APPLICANT:  MERUELO, DANIEL
;    APPLICANT:  YOSHIMOTO, TAKAYUKI
;    TITLE OF INVENTION:  Human Retrovirus Receptor and DNA Coding Therefor
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patent In Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/132,990A
;      FILING DATE:  07-OCT-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/084,729
;      FILING DATE:  29-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/05569
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/899,075
;      FILING DATE:  11-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/806,178
;      FILING DATE:  13-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/627,950
;      FILING DATE:  14-DEC-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  8105-004-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-8864
;      TELEX:  66441 PENNIE
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2157 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  148..2034
US-08-132-990A-7


  Query Match             1.1%;  Score 16;  DB 3;  Length 2157;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy     450 caaagtcctgctcaac 465
           ||||||||||||||||
Db     156 CAAAGTCCTGCTCAAC 171
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Search completed: April 14, 2000, 18:27:45
Job time: 7077 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 14, 2000, 17:42:31 ; Search time 1303.77 Seconds
(without alignments)
4039.862 Million cell updates/sec

Title: US-09-388-090-3
Perfect score: 1395
Sequence: 1 gtgttcaaaaaataccaata.....tcagggcaagtccccgtcaa 1395

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4538634 seqs, 1887831982 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9077268

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Listing first 1000 summaries

Database : EST:*
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2: em_est2:*
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5: em_est5:*
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101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	1.4	200	27	C03492	C03492 C03492 Huma

	2	20	1.4	304	40	AA958603 AA958603 ua15e07.r
	3	20	1.4	329	44	AI324092 AI324092 mh04b12.x
	4	20	1.4	445	34	AA475998 AA475998 vh25h10.r
c	5	20	1.4	458	27	AA013893 AA013893 mh04b12.r
	6	20	1.4	482	33	AA447906 AA447906 zx11b06.r
c	7	20	1.4	557	44	AI322461 AI322461 mh04b12.y
c	8	19	1.4	354	37	AA672965 AA672965 vn48b11.r
	9	19	1.4	508	47	AI538510 AI538510 td07e06.x
c	10	19	1.4	633	28	AA106132 AA106132 mm20f05.r
	11	18	1.3	63	51	AI756231 AI756231 ea41d11.y
	12	18	1.3	330	20	D37319 D37319 CELK043HXF
	13	18	1.3	360	24	D68430 D68430 CELK131C4F
	14	18	1.3	371	48	AI585708 AI585708 mq93b02.y
	15	18	1.3	420	29	AA140161 AA140161 mq93b02.r
c	16	18	1.3	433	45	AI372103 AI372103 am78a04.x
	17	18	1.3	438	103	AQ447358 AQ447358 mgxb0006L
c	18	18	1.3	462	29	AA159654 AA159654 zo86b10.r
	19	18	1.3	469	88	AQ853281 AQ853281 LMAJFV1_1
c	20	18	1.3	471	89	AQ911814 AQ911814 LMAJFV1_1
	21	18	1.3	488	91	AQ136002 AQ136002 HS_3055_B
	22	18	1.3	491	99	AQ216877 AQ216877 HS_3253_B
	23	18	1.3	502	103	AQ449287 AQ449287 mgxb0023K
c	24	18	1.3	551	21	T62818 T62818 yc70b04.s1
	25	18	1.3	564	63	AI947590 AI947590 603024D11
c	26	18	1.3	597	100	AQ276833 AQ276833 CITBI-E1-
c	27	18	1.3	619	103	AQ469404 AQ469404 CITBI-E1-
c	28	18	1.3	645	42	AI107025 AI107025 GH06310.3
c	29	18	1.3	668	104	AQ543740 AQ543740 RPCI-11-3
c	30	18	1.3	693	104	AQ545949 AQ545949 CITBI-E1-
	31	18	1.3	723	91	AQ158994 AQ158994 nbxb0012L
c	32	18	1.3	756	34	AA519798 AA519798 TgESTzz35
	33	18	1.3	756	91	AQ163302 AQ163302 mgxb0023P
	34	18	1.3	806	45	AI356645 AI356645 qy16d12.x
	35	18	1.3	893	80	AF075974 AF075974 Salmonell
	36	18	1.3	901	80	AF075966 AF075966 Salmonell
	37	18	1.3	973	80	AF075860 AF075860 Salmonell
	38	18	1.3	977	80	AF075892 AF075892 Salmonell
	39	18	1.3	1050	79	CNS00GRM AL072458 Drosophil
	40	18	1.3	1076	80	AF075862 AF075862 Salmonell
c	41	18	1.3	1089	28	U70074 U70074 HSU70074 Hu
c	42	18	1.3	1101	79	CNS0012O AL056113 Drosophil
	43	17	1.2	73	40	AA931149 AA931149 oo70c09.s
c	44	17	1.2	106	27	AA024642 AA024642 ze79a05.r
c	45	17	1.2	117	42	AI126325 AI126325 qd82c03.x
	46	17	1.2	124	45	AI355872 AI355872 qu02f10.x
c	47	17	1.2	127	90	AQ025988 AQ025988 EP(2)0380
c	48	17	1.2	127	90	AQ026416 AQ026416 ms(2)0649
	49	17	1.2	133	64	AW073768 AW073768 xb12g08.x
	50	17	1.2	135	47	AI496080 AI496080 sa95f03.y
	51	17	1.2	145	26	W85266 W85266 mf45h12.r1
	52	17	1.2	148	60	AI794914 AI794914 sb73e01.y
c	53	17	1.2	151	74	AW225218 AW225218 687054C04
	54	17	1.2	193	20	D12142 D12142 HUM000S240
c	55	17	1.2	193	62	AI905624 AI905624 CM-BT094-
	56	17	1.2	211	63	AW009718 AW009718 ws86e10.x
	57	17	1.2	224	62	AI905837 AI905837 IL-BT099-
	58	17	1.2	258	46	AI441034 AI441034 sa58e08.y
c	59	17	1.2	286	31	AA302590 AA302590 EST15812
	60	17	1.2	289	61	AI833248 AI833248 at76e07.x
	61	17	1.2	290	32	AA341610 AA341610 EST47198
c	62	17	1.2	294	32	AA340069 AA340069 EST45219
c	63	17	1.2	295	70	AV224407 AV224407
c	64	17	1.2	296	32	AA366765 AA366765 EST77750
	65	17	1.2	298	45	AI351243 AI351243 qt47e05.x
c	66	17	1.2	298	90	AQ073531 AQ073531 EP(2)2369
	67	17	1.2	298	99	AQ254813 AQ254813 EP(2)0816
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	70	17	1.2	300	90	AQ073299 AQ073299 l(2)10607
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	72	17	1.2	304	90	AQ025925 AQ025925 l(2)k1011
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c	74	17	1.2	312	28	AA092926 AA092926 m0611.seq
	75	17	1.2	313	46	AI443030 AI443030 sa31a05.y
	76	17	1.2	313	74	AW176044 AW176044 QV0-BT010
	77	17	1.2	319	33	AA385242 AA385242 EST98891
c	78	17	1.2	322	32	AA362064 AA362064 EST71717
	79	17	1.2	326	25	N77431 N77431 yz31g08.r1
c	80	17	1.2	328	50	AI674135 AI674135 wd08b02.x
c	81	17	1.2	328	64	AW016622 AW016622 UI-H-BI0p
	82	17	1.2	329	64	AW050788 AW050788 wz21e04.x
c	83	17	1.2	331	31	AA304896 AA304896 EST175920
	84	17	1.2	336	47	AI496576 AI496576 sb13e08.y
	85	17	1.2	339	47	AI494969 AI494969 sa93c10.y
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	87	17	1.2	342	46	AI437993 AI437993 sa34f01.y
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	94	17	1.2	356	40	AA920819 AA920819 vy83a11.r
c	95	17	1.2	360	28	C13485 C13485 Yuji
	96	17	1.2	360	36	C63387 C63387 Yuji
	97	17	1.2	360	36	C65143 C65143 Yuji
	98	17	1.2	360	62	AV186467 AV186467
	99	17	1.2	360	62	AV192074 AV192074
	100	17	1.2	360	62	AV198387 AV198387
	101	17	1.2	361	47	AI495656 sb11f08.y
c	102	17	1.2	363	44	AI277668 AI277668 ql78f03.x
c	103	17	1.2	363	60	AI796907 AI796907 we23g01.x
	104	17	1.2	370	73	AW170669 AW170669 x185g05.x
	105	17	1.2	376	104	AQ513981 AQ513981 HS_5179_B
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	107	17	1.2	379	49	AI628510 AI628510 ty94h01.x
c	108	17	1.2	384	30	AA225545 AA225545 nc08b08.s
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	110	17	1.2	392	100	AQ262683 AQ262683 CITBI-E1-
	111	17	1.2	393	45	AI356408 AI356408 qz26g10.x
	112	17	1.2	393	63	AI980829 AI980829 pat.pk003
c	113	17	1.2	395	61	AI827179 AI827179 wk90c09.x
c	114	17	1.2	396	41	AI008558 AI008558 EST203009
	115	17	1.2	398	36	AA645936 AA645936 vn11d12.r
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c	117	17	1.2	401	24	N25993 N25993 yx88d06.s1
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	120	17	1.2	403	20	Z46535 Z46535 ATTS4279 Ve
c	121	17	1.2	403	22	R75793 R75793 yl21f09.r1
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	128	17	1.2	409	46	AI454973 AI454973 LD01523.5
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	131	17	1.2	411	51	AI717148 AI717148 UI-R-Y0-a
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c	133	17	1.2	413	49	AI636198 AI636198 tz06f08.x
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c	135	17	1.2	414	40	AA921758 AA921758 om43g04.s
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	151	17	1.2	429	39	AA826878 AA826878 nr90e06.s
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	154	17	1.2	432	26	W72838 W72838 zd57g12.s1
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c	156	17	1.2	434	24	H78162 H78162 yu86h10.r1
c	157	17	1.2	436	26	W72837 W72837 zd57g12.r1
	158	17	1.2	436	63	AW006216 AW006216 wz93g03.x
	159	17	1.2	436	74	AW192193 AW192193 xl81c08.x
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c	161	17	1.2	438	44	AI261769 AI261769 qk10c02.x
c	162	17	1.2	440	41	AI058424 AI058424 UI-R-C1-k
c	163	17	1.2	442	44	AI292334 AI292334 qm77b10.x
	164	17	1.2	442	88	AQ849884 AQ849884 LMAJFV1_1
	165	17	1.2	443	42	AI127172 AI127172 qb99a08.x
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c	167	17	1.2	446	43	AI185820 AI185820 qe49h04.x
	168	17	1.2	447	38	AA745977 AA745977 ob18g03.s
	169	17	1.2	447	39	AA822994 AA822994 vw39d09.r
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c	171	17	1.2	450	25	N62285 N62285 yz90b12.s1
	172	17	1.2	450	63	AI943549 AI943549 BSBmMFSZ4
c	173	17	1.2	455	23	H50679 H50679 yp86h01.s1
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c	176	17	1.2	456	63	AW005143 AW005143 wv80c03.x
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	179	17	1.2	457	72	AW162476 AW162476 au66g06.x
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	183	17	1.2	459	33	AA424101 AA424101 zv80c05.r
c	184	17	1.2	459	41	AI062297 AI062297 GH01453.5
c	185	17	1.2	460	29	AA173647 AA173647 zp03h04.r
	186	17	1.2	460	46	AI406459 AI406459 EST234745
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c	188	17	1.2	463	60	AI802061 AI802061 tx29h01.x
c	189	17	1.2	467	60	AI796951 AI796951 we25b10.x
	190	17	1.2	468	87	AQ805033 AQ805033 HS_3083_A
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	192	17	1.2	472	64	AW028011 AW028011 wv61b09.x
	193	17	1.2	472	99	AQ196276 AQ196276 RPCI11-61
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c	195	17	1.2	475	48	AI566228 AI566228 tq70a09.x
	196	17	1.2	476	39	AA822985 AA822985 vw39c10.r
c	197	17	1.2	476	100	AQ323168 AQ323168 RPCI11-10
	198	17	1.2	478	102	AQ349756 AQ349756 RPCI11-12
c	199	17	1.2	479	35	AA583028 AA583028 nn80e02.s
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	203	17	1.2	484	39	AA823851 AA823851 vt08e07.r
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	205	17	1.2	485	88	AQ846618 AQ846618 LMAJFV1_1
	206	17	1.2	487	46	AI399464 AI399464 NCSP4G11T
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c	209	17	1.2	496	61	AL043942 AL043942 DKFZp434F
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	212	17	1.2	498	88	AQ875479 AQ875479 V125H1 mT
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	214	17	1.2	502	39	AA881220 AA881220 vx10c05.r
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c	217	17	1.2	506	69	AW141797 AW141797 EST291890
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	219	17	1.2	509	34	AA462995 AA462995 vg70c04.r
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	221	17	1.2	511	35	AA562784 AA562784 vl44g03.r
c	222	17	1.2	511	105	AQ665829 AQ665829 HS_5372_B
	223	17	1.2	512	51	AI713183 AI713183 UI-R-Y0-a
c	224	17	1.2	515	103	AQ448485 AQ448485 mgxb0020F
c	225	17	1.2	516	39	AA876066 AA876066 ob93a09.s
	226	17	1.2	519	36	AA636495 AA636495 vr18e10.r
	227	17	1.2	520	37	AA719302 AA719302 zh35b11.s
c	228	17	1.2	522	60	AI796182 AI796182 wh43f05.x
	229	17	1.2	523	100	AQ295445 AQ295445 HS_3034_B
c	230	17	1.2	527	73	AW167553 AW167553 xn55g02.x
	231	17	1.2	530	88	AQ848057 AQ848057 LMAJFV1_1
	232	17	1.2	537	102	AQ376675 AQ376675 RPCI-11-1
c	233	17	1.2	543	48	AI591148 AI591148 tw86a04.x
c	234	17	1.2	544	79	CNS00N6L AL081531 Arabidops
	235	17	1.2	551	105	AQ663921 AQ663921 HS_2171_B
	236	17	1.2	552	43	AI102258 AI102258 EST211547
c	237	17	1.2	554	38	AA743709 AA743709 ny92f03.s
	238	17	1.2	554	63	AI955196 AI955196 wx31b04.x
c	239	17	1.2	557	45	AI378295 AI378295 tc43h09.x
	240	17	1.2	557	88	AQ855270 AQ855270 CpG1897A
c	241	17	1.2	559	41	AI023165 AI023165 ow66c02.s
c	242	17	1.2	559	63	AW007110 AW007110 wt09c09.x
	243	17	1.2	564	105	AQ655922 AQ655922 Sheared D
	244	17	1.2	565	74	AV388115 AV388115 AV388115
	245	17	1.2	569	64	AW042303 AW042303 614026G07
c	246	17	1.2	576	30	AA242244 AA242244 mw25c10.r
c	247	17	1.2	587	50	AI672891 AI672891 we73g06.x
	248	17	1.2	590	105	AQ633932 AQ633932 RPCI-11-4
	249	17	1.2	596	34	AA517392 AA517392 vh99h07.r
	250	17	1.2	600	74	AW175086 AW175086 fi32b02.y
c	251	17	1.2	602	43	AI179329 AI179329 EST223024
c	252	17	1.2	602	49	AI649752 AI649752 496009C09
	253	17	1.2	613	39	AA872875 AA872875 oh57h01.s
c	254	17	1.2	622	28	AA099900 AA099900 zk87e09.r
	255	17	1.2	625	28	AA098827 AA098827 zn45a02.r
c	256	17	1.2	631	36	AA660699 AA660699 00588 MtR
c	257	17	1.2	631	69	AW141292 AW141292 EST291333
	258	17	1.2	632	100	AQ287526 AQ287526 nbxb0030M
c	259	17	1.2	633	27	AA045236 AA045236 zk65g03.s
	260	17	1.2	635	39	AA846530 AA846530 aj56f03.s
c	261	17	1.2	640	64	AW018930 AW018930 fd61h05.y
	262	17	1.2	643	105	AQ638249 AQ638249 927P1-11H
c	263	17	1.2	645	61	AL038359 AL038359 DKFZp566L
	264	17	1.2	654	45	AA799313 AA799313 EST188810
c	265	17	1.2	671	100	AQ287833 AQ287833 nbxb0031M
c	266	17	1.2	692	105	AQ641338 AQ641338 RPCI93-Dp
c	267	17	1.2	697	36	AA643031 AA643031 nr57b07.s
	268	17	1.2	699	105	AQ638258 AQ638258 927P1-11H
	269	17	1.2	710	82	AQ689558 AQ689558 nbxb0079L
c	270	17	1.2	712	43	AI176730 AI176730 EST220323
	271	17	1.2	716	81	B77585 B77585 T27B24TR TA
c	272	17	1.2	733	80	AF075876 AF075876 Salmonell
	273	17	1.2	736	61	AL037328 AL037328 DKFZp564E
	274	17	1.2	737	104	AQ575421 AQ575421 nbxb0087E
	275	17	1.2	751	64	AW027541 AW027541 wv74d09.x
	276	17	1.2	752	49	AI664723 AI664723 TENG0684
	277	17	1.2	753	42	AI092271 AI092271 oz97e05.x
	278	17	1.2	759	89	AQ916509 AQ916509 nbeb0065E
	279	17	1.2	762	64	AL038360 AL038360 DKFZp566L
	280	17	1.2	762	100	AQ327052 AQ327052 nbxb0040G
	281	17	1.2	778	63	AW013050 AW013050 Odt-0097
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	283	17	1.2	835	34	AA522522 AA522522 ni38d02.s
	284	17	1.2	919	79	CNS00CSW AL059697 Drosophil
	285	17	1.2	929	79	CNS008CZ AL051517 Drosophil
	286	17	1.2	932	79	CNS0048C AL066389 Drosophil
	287	17	1.2	932	88	AQ890086 AQ890086 HS_4831_B
	288	17	1.2	947	79	CNS00D31 AL060567 Drosophil
	289	16	1.1	52	43	AI203654 AI203654 qf48e05.x
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	292	16	1.1	167	64	AW074095 AW074095 xb07f03.x
	293	16	1.1	185	37	R83937 R83937 15896 Lambd

	294	16	1.1	188	26	W35479	W35479 139 Mouse V
	295	16	1.1	193	103	AQ485008	AQ485008 RPCI-11-2
c	296	16	1.1	195	59	AV093620	AV093620 AV093620
	297	16	1.1	195	74	AW219735	AW219735 EST302217
	298	16	1.1	200	42	AI149336	qc76h03.x
	299	16	1.1	203	69	AV206565	AV206565 AV206565
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	301	16	1.1	213	25	N48947	N48947 yy76d10.r1
	302	16	1.1	214	31	AA308883	AA308883 EST179687
	303	16	1.1	216	50	AI708431	AI708431 as97b12.x
c	304	16	1.1	218	71	AV256058	AV256058 AV256058
	305	16	1.1	219	50	AV039825	AV039825 AV039825
	306	16	1.1	219	88	AQ846781	AQ846781 LMAJFV1_1
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	308	16	1.1	229	59	AV067339	AV067339 AV067339
c	309	16	1.1	235	70	AV241809	AV241809 AV241809
c	310	16	1.1	237	39	AA885632	AA885632 oj32a10.s
c	311	16	1.1	241	63	AI946380	AI946380 bs24f07.y
	312	16	1.1	242	43	C99795	C99795 C99795 YAC
	313	16	1.1	242	74	AV380962	AV380962 AV380962
	314	16	1.1	243	20	T14448	T14448 SMEST0109 S
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	316	16	1.1	246	30	AA266274	AA266274 mz63f05.r
	317	16	1.1	247	34	AA466846	AA466846 ve92g09.r
c	318	16	1.1	249	74	AV376746	AV376746 AV376746
	319	16	1.1	252	73	AV338944	AV338944 AV338944
c	320	16	1.1	254	48	AI572526	AI572526 te38h07.x
c	321	16	1.1	254	71	AV323763	AV323763 AV323763
	322	16	1.1	255	24	H97184	H97184 yx03h09.s1
c	323	16	1.1	258	29	AA127054	AA127054 zn28f09.s
c	324	16	1.1	259	59	AV095548	AV095548 AV095548
c	325	16	1.1	262	21	T97160	T97160 ye50c12.r1
	326	16	1.1	262	28	C15514	C15514 C15514 Clon
	327	16	1.1	266	71	AV278197	AV278197 AV278197
	328	16	1.1	267	100	AQ264612	AQ264612 CITBI-E1-
	329	16	1.1	269	59	AV082003	AV082003 AV082003
	330	16	1.1	271	34	AA489615	AA489615 ae32h12.r
c	331	16	1.1	272	70	AW154961	AW154961 614092H12
c	332	16	1.1	273	73	AV341111	AV341111 AV341111
c	333	16	1.1	274	36	C73800	C73800 C73800 Rice
	334	16	1.1	277	51	AV052860	AV052860 AV052860
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	336	16	1.1	279	38	AA772123	AA772123 ai40c12.s
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c	338	16	1.1	279	50	AV039520	AV039520 AV039520
	339	16	1.1	280	82	AQ667091	AQ667091 HS_2107_A
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	342	16	1.1	284	29	AA127053	AA127053 zn28f09.r
c	343	16	1.1	284	39	AA882981	AA882981 TENS0558
c	344	16	1.1	284	61	AI856565	AI856565 sb39a05.y
c	345	16	1.1	284	72	AV290599	AV290599 AV290599
	346	16	1.1	285	23	R97430	R97430 yq53h01.s1
	347	16	1.1	286	62	AI874226	AI874226 tz63a05.x
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	349	16	1.1	288	69	AV214645	AV214645 AV214645
	350	16	1.1	290	60	AV139975	AV139975 AV139975
c	351	16	1.1	293	60	AV119054	AV119054 AV119054
c	352	16	1.1	296	59	AV118435	AV118435 AV118435
	353	16	1.1	297	60	AV118938	AV118938 AV118938
	354	16	1.1	297	64	AW089750	AW089750 xd07e12.x
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	356	16	1.1	303	79	CNS00O6Q	AL082832 Arabidops
	357	16	1.1	304	69	AW135710	AW135710 UI-H-BI1-
c	358	16	1.1	304	81	B83478	B83478 RPCI11-15C2
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c	360	16	1.1	311	69	AV215348	AV215348 AV215348
	361	16	1.1	312	31	AA308981	AA308981 EST179788
c	362	16	1.1	313	62	AI928295	AI928295 wp12a11.x
c	363	16	1.1	314	41	AU007657	AU007657 AU007657
c	364	16	1.1	315	105	AQ640238	AQ640238 927P1-2F6
	365	16	1.1	317	87	AQ817313	AQ817313 HS_5281_A
	366	16	1.1	320	42	AI099654	AI099654 34380 Lam
c	367	16	1.1	320	48	AI582808	AI582808 tn36a05.x
	368	16	1.1	320	104	AQ529847	AQ529847 RPCI-11-3
c	369	16	1.1	325	24	H82595	H82595 yv77g07.r1
c	370	16	1.1	327	20	Z25652	Z25652 ATTS1117 Ve
c	371	16	1.1	327	32	AA366349	AA366349 EST77284
c	372	16	1.1	331	90	AQ031642	AQ031642 HS_2225_B
	373	16	1.1	333	90	AQ009196	AQ009196 CIT-HFP-2
	374	16	1.1	334	33	AA393011	AA393011 LD03296.5
	375	16	1.1	337	27	AA038448	AA038448 mi92a07.r
	376	16	1.1	337	60	AV119872	AV119872 AV119872
	377	16	1.1	338	39	AA833189	AA833189 ud02h03.r
	378	16	1.1	339	90	AQ070924	AQ070924 HS_2268_A
c	379	16	1.1	342	29	AA142321	AA142321 JM00M038.
	380	16	1.1	345	34	C25363	C25363 C25363 Rice
	381	16	1.1	345	82	AQ676784	AQ676784 HS_5496_B
	382	16	1.1	347	40	AA951481	AA951481 LD31959.5
	383	16	1.1	347	62	AV188650	AV188650 AV188650
c	384	16	1.1	347	63	AI945870	AI945870 bs17g09.y
c	385	16	1.1	349	59	AV117032	AV117032 AV117032
c	386	16	1.1	351	81	B54075	B54075 CIT-HSP-201
	387	16	1.1	353	30	AA201832	AA201832 LD03743.5
c	388	16	1.1	353	47	AI467932	AI467932 tj84c04.x
	389	16	1.1	355	21	R14564	R14564 yf83e10.r1
	390	16	1.1	356	33	AA391750	AA391750 LD10801.5
c	391	16	1.1	357	88	AQ841300	AQ841300 T136443b
	392	16	1.1	357	91	AQ091904	AQ091904 HS_3014_B
	393	16	1.1	358	20	Z43649	Z43649 HSC1HF091 n
c	394	16	1.1	358	23	H41275	H41275 yp67b11.s1
	395	16	1.1	358	44	AI308725	AI308725 SWOvAFCAP
c	396	16	1.1	359	81	B76220	B76220 RPCI11-14A1
	397	16	1.1	360	36	C62190	C62190 C62190 Yuji
	398	16	1.1	360	36	C66985	C66985 C66985 Yuji
	399	16	1.1	361	51	AI750952	AI750952 cn06g02.y
	400	16	1.1	362	33	AA439053	AA439053 LD13491.5
	401	16	1.1	362	43	AI220074	AI220074 qg84d10.x
c	402	16	1.1	363	21	T66808	T66808 ya50a11.r1
	403	16	1.1	363	23	H42280	H42280 yo63d01.r1
c	404	16	1.1	365	36	AA639273	AA639273 ns04h10.r
	405	16	1.1	365	79	FR0009261	AL000547 F.rubripe
c	406	16	1.1	369	81	B50113	B50113 CIT978SK-44
c	407	16	1.1	370	21	T84502	T84502 yd49f04.r1
c	408	16	1.1	372	45	AI396263	AI396263 487013F10
	409	16	1.1	373	38	AA541038	AA541038 LD20821.5
	410	16	1.1	373	40	Z19071	Z19071 HSDHEEB09 S
c	411	16	1.1	373	46	AI418991	AI418991 tf43e08.x
c	412	16	1.1	373	62	AI928292	AI928292 wp12a08.x
c	413	16	1.1	374	44	AI323838	AI323838 mt66b10.x
c	414	16	1.1	374	61	AI827625	AI827625 wf32b10.x
	415	16	1.1	375	21	T93973	T93973 ye29a04.r1
	416	16	1.1	376	64	AW091328	AW091328 614092H12
c	417	16	1.1	379	47	AI490102	AI490102 EST248441
	418	16	1.1	380	27	C09398	C09398 C09398 Yuji
	419	16	1.1	380	41	AI019143	AI019143 ub20a09.r
	420	16	1.1	381	100	AQ297279	AQ297279 HS_3051_A
c	421	16	1.1	382	62	AI898249	AI898249 EST267692
c	422	16	1.1	385	29	AA133576	AA133576 zo14f12.r
	423	16	1.1	386	21	R17172	R17172 yg11a06.r1
c	424	16	1.1	386	43	AI193885	AI193885 qe80e06.x
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	426	16	1.1	388	33	AA442642	AA442642 zv59g10.r
	427	16	1.1	388	42	AI094749	AI094749 qa08h11.x
	428	16	1.1	388	81	B87719	B87719 RPCI11-30D1
	429	16	1.1	389	47	AI494189	AI494189 ti14h02.y
	430	16	1.1	389	64	AW017204	AW017204 EST272626
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c	432	16	1.1	391	47	AI488400	AI488400 EST246722
c	433	16	1.1	393	35	AA538848	AA538848 LD18470.5
	434	16	1.1	393	39	AA820139	AA820139 LD23606.5
	435	16	1.1	393	87	AQ772752	AQ772752 HS_2019_B
	436	16	1.1	393	99	AQ235351	AQ235351 HS_2055_A
	437	16	1.1	394	88	AQ854618	AQ854618 nbxb0080J
	438	16	1.1	398	34	AA472480	AA472480 vh07b03.r
c	439	16	1.1	398	37	T43614	T43614 6877 Lambda

c 440	16	1.1	399	31	AA286767	AA286767 zs51d06.r
c 441	16	1.1	400	46	AI399304	AI399304 NCW07A3T3
442	16	1.1	401	29	AA154765	AA154765 mt66b10.r
443	16	1.1	402	42	AI118748	AI118748 uc13a06.r
c 444	16	1.1	403	91	AQ115777	AQ115777 RPCI11-52
445	16	1.1	404	26	W97216	W97216 mg08e02.r1
446	16	1.1	404	34	AA536616	AA536616 LD17388.5
c 447	16	1.1	405	64	AL120877	AL120877 DKFZp762L
448	16	1.1	405	90	AQ016864	AQ016864 CIT-HSP-2
c 449	16	1.1	407	42	AI146879	AI146879 oy22g09.s
450	16	1.1	408	30	AA203034	AA203034 LD03496.5
c 451	16	1.1	408	81	B62642	B62642 T22M16TF TA
c 452	16	1.1	409	40	AA965984	AA965984 r8g07a1.r
c 453	16	1.1	413	87	AQ794203	AQ794203 nbxb0052E
c 454	16	1.1	415	74	AV393174	AV393174 AV393174
455	16	1.1	415	91	AQ090792	AQ090792 HS_3011_B
c 456	16	1.1	416	24	H63134	H63134 yr48g04.s1
457	16	1.1	416	60	AI800154	AI800154 tr23a08.x
c 458	16	1.1	417	90	AQ045104	AQ045104 RPCI11-34
c 459	16	1.1	418	27	AA049953	AA049953 mj38e11.r
c 460	16	1.1	418	62	AI878079	AI878079 fc57b11.y
c 461	16	1.1	419	27	AA049960	AA049960 mj38g11.r
462	16	1.1	419	45	AI383412	AI383412 tc97d08.x
c 463	16	1.1	420	31	AA310554	AA310554 EST181358
c 464	16	1.1	420	62	AI894692	AI894692 EST264135
465	16	1.1	422	50	AI699292	AI699292 wa67a04.x
c 466	16	1.1	423	100	AQ321950	AQ321950 RPCI11-10
467	16	1.1	424	88	AQ852769	AQ852769 LMAJFV1_1
468	16	1.1	426	31	AA282606	AA282606 zs90a05.r
c 469	16	1.1	427	23	H41411	H41411 yp72c05.s1
c 470	16	1.1	427	40	AA922280	AA922280 om46g11.s
471	16	1.1	427	88	AQ889542	AQ889542 HS_3188_B
472	16	1.1	428	43	AI225101	AI225101 qi32f03.x
c 473	16	1.1	429	36	AA632061	AA632061 np70e09.s
474	16	1.1	429	99	AQ206905	AQ206905 HS_3238_B
c 475	16	1.1	433	62	AI894670	AI894670 EST264113
476	16	1.1	434	38	AA812252	AA812252 nr82b11.s
c 477	16	1.1	434	69	AV383024	AV383024 AV383024
c 478	16	1.1	434	99	AQ234513	AQ234513 HS_2052_B
479	16	1.1	435	22	R25683	R25683 yg44c12.r2
480	16	1.1	437	104	AQ517442	AQ517442 HS_5119_B
481	16	1.1	438	25	W04974	W04974 za42d01.r1
482	16	1.1	438	82	AQ737932	AQ737932 HS_2017_B
c 483	16	1.1	439	21	T80697	T80697 yd23c04.r1
484	16	1.1	439	41	AI047675	AI047675 uh81f04.r
c 485	16	1.1	439	42	AF074726	AF074726 AF074726
c 486	16	1.1	439	48	AI566932	AI566932 tn25b02.x
c 487	16	1.1	439	64	AW083818	AW083818 xc35f02.x
c 488	16	1.1	439	104	AQ561655	AQ561655 HS_5206_A
489	16	1.1	440	88	AQ852393	AQ852393 LMAJFV1_1
c 490	16	1.1	441	21	R20975	R20975 yg06e08.r1
491	16	1.1	442	34	AA532899	AA532899 nj18d05.s
492	16	1.1	443	25	N77807	N77807 zb16a04.s1
c 493	16	1.1	445	23	H44640	H44640 yp20a05.r1
c 494	16	1.1	448	29	AA178472	AA178472 mt16f07.r
495	16	1.1	448	31	AA291297	AA291297 zs18e07.s
496	16	1.1	448	87	AQ777821	AQ777821 HS_2024_B
c 497	16	1.1	449	105	AQ660706	AQ660706 Sheared D
c 498	16	1.1	450	44	AI298185	AI298185 qm92h02.x
499	16	1.1	450	47	AI542799	AI542799 SD09264.5
500	16	1.1	451	30	AA258248	AA258248 zs33e07.s
501	16	1.1	452	37	AA704897	AA704897 zj82a05.s
502	16	1.1	455	25	N59538	N59538 yv76c07.s1
c 503	16	1.1	455	42	AI123667	AI123667 oo16d02.x
504	16	1.1	457	30	AA214786	AA214786 mu81c07.r
505	16	1.1	457	39	AA820459	AA820459 LD24202.5
506	16	1.1	457	39	C85918	C85918 C85918 Mous
507	16	1.1	458	82	AQ713878	AQ713878 HS_2129_B
508	16	1.1	458	100	AQ316940	AQ316940 CITBI-E1-
c 509	16	1.1	459	31	AA287068	AA287068 zt20d08.r
510	16	1.1	459	39	AA846382	AA846382 aj55e05.s
511	16	1.1	460	45	AA859439	AA859439 UI-R-A0-b
c 512	16	1.1	462	23	H39685	H39685 yo52c06.r1
c 513	16	1.1	464	42	AI083728	AI083728 qf19d03.x
c 514	16	1.1	464	74	AW201529	AW201529 sf04c04.y
c 515	16	1.1	464	91	AQ126320	AQ126320 HS_3037_B
516	16	1.1	465	46	AA998141	AA998141 UI-R-C0-i
c 517	16	1.1	467	30	AA212334	AA212334 mu78e05.r
518	16	1.1	467	47	AI510465	AI510465 mp97d09.y
c 519	16	1.1	467	88	AQ866488	AQ866488 nbeb0028M
520	16	1.1	468	46	AI461125	AI461125 sa75d03.y
c 521	16	1.1	469	34	AA458650	AA458650 aa16c07.s
c 522	16	1.1	469	74	AW201559	AW201559 sf04f02.y
523	16	1.1	470	45	AI362952	AI362952 qy87f08.x
c 524	16	1.1	470	64	AW084586	AW084586 wz26h09.x
c 525	16	1.1	470	88	AQ881958	AQ881958 HS_5323_A
c 526	16	1.1	473	47	AI488044	AI488044 EST246366
527	16	1.1	473	91	AQ109936	AQ109936 CIT-HSP-2
c 528	16	1.1	474	39	AA824610	AA824610 oc83f11.s
c 529	16	1.1	474	48	AI622223	AI622223 486038B04
530	16	1.1	476	25	N70411	N70411 za61b11.s1
531	16	1.1	476	47	AI513631	AI513631 LD45833.5
c 532	16	1.1	477	45	AI338219	AI338219 qt41f05.x
c 533	16	1.1	477	99	AQ233981	AQ233981 HS_2053_A
534	16	1.1	478	40	AA949961	AA949961 LD28543.5
c 535	16	1.1	478	60	AV119858	AV119858 AV119858
c 536	16	1.1	479	74	AV396004	AV396004 AV396004
537	16	1.1	479	99	AQ208862	AQ208862 HS_3056_B
c 538	16	1.1	480	29	AA158523	AA158523 zo72d09.s
c 539	16	1.1	480	41	AI035516	AI035516 ub48c11.r
c 540	16	1.1	480	90	AQ073076	AQ073076 EP(3)3633
541	16	1.1	481	47	AI475830	AI475830 tc87a09.x
542	16	1.1	481	47	AI516685	AI516685 LD42655.5
c 543	16	1.1	481	81	B44856	B44856 HS-1060-A1-
544	16	1.1	482	46	AI456208	AI456208 LD36079.5
c 545	16	1.1	482	62	AI899810	AI899810 sb94b01.y
546	16	1.1	483	62	AI927347	AI927347 wn49f03.x
c 547	16	1.1	484	21	R10794	R10794 yf36e02.r1
c 548	16	1.1	485	46	AI405307	AI405307 GH25264.5
c 549	16	1.1	487	21	T83350	T83350 ye03d02.s1
550	16	1.1	487	23	H49657	H49657 yo23a04.r1
c 551	16	1.1	488	88	AQ849736	AQ849736 LMAJFV1_1
552	16	1.1	489	63	AI976899	AI976899 EST271581
553	16	1.1	489	99	AQ179521	AQ179521 HS_3169_B
554	16	1.1	489	103	AQ502171	AQ502171 V8B11 mTn
555	16	1.1	490	40	AA940893	AA940893 LD23215.5
c 556	16	1.1	491	102	AQ399124	AQ399124 mgxb0006F
c 557	16	1.1	492	104	AQ570746	AQ570746 HS_5355_B
558	16	1.1	492	105	AQ612864	AQ612864 HS_5116_A
c 559	16	1.1	493	34	AA478883	AA478883 zv19g12.r
c 560	16	1.1	493	82	AQ692599	AQ692599 HS_5433_A
c 561	16	1.1	494	38	AA785424	AA785424 q7c05a1.r
562	16	1.1	494	39	AA902079	AA902079 NCP5E5T7
c 563	16	1.1	494	88	AQ848684	AQ848684 LMAJFV1_1
564	16	1.1	495	40	AA948788	AA948788 LD27419.5
c 565	16	1.1	495	79	FR0023707	AL016563 F.rubripe
c 566	16	1.1	497	26	W47960	W47960 mc87d01.r1
567	16	1.1	497	38	AA392315	AA392315 LD11140.5
c 568	16	1.1	497	38	AA788270	AA788270 r6d05a1.r
569	16	1.1	498	40	AA949851	AA949851 LD29895.5
c 570	16	1.1	498	74	AV394515	AV394515 AV394515
571	16	1.1	498	74	AW205581	AW205581 UI-H-BI1-
c 572	16	1.1	500	36	AA641620	AA641620 nr80a07.s
573	16	1.1	501	100	AQ340412	AQ340412 HS_2226_A
c 574	16	1.1	502	48	AI560775	AI560775 tn22c02.x
575	16	1.1	504	64	AW019258	AW019258 fd61f12.x
c 576	16	1.1	504	87	AQ784629	AQ784629 HS_3193_B
c 577	16	1.1	504	88	AQ853015	AQ853015 LMAJFV1_1
c 578	16	1.1	504	99	AQ172611	AQ172611 HS_3197_A
579	16	1.1	504	100	AQ302145	AQ302145 HS_3126_B
580	16	1.1	504	103	AQ425525	AQ425525 CITBI-E1-
581	16	1.1	505	62	AI891122	AI891122 wn28g10.x
c 582	16	1.1	506	103	AQ447504	AQ447504 mgxb0007L
583	16	1.1	507	44	AI262484	AI262484 qk41c12.x
c 584	16	1.1	507	74	AV394960	AV394960 AV394960
585	16	1.1	508	99	AQ193332	AQ193332 HS_3065_A

	586	16	1.1	510	82	AQ694541 AQ694541 HS_5485_A
	587	16	1.1	512	40	AA988109 AA988109 os07a12.s
c	588	16	1.1	512	74	AV394283 AV394283
	589	16	1.1	513	44	AI278442 AI278442 qm53d01.x
c	590	16	1.1	514	47	AI494909 AI494909 sa92e02.y
	591	16	1.1	514	62	AI886863 AI886863 wk29e12.x
	592	16	1.1	514	81	B27698 B27698 T14O3TRB TA
c	593	16	1.1	515	61	AI813494 AI813494 wj64f04.x
c	594	16	1.1	515	74	AW200000 AW200000 da10d05.y
	595	16	1.1	515	104	AQ526647 AQ526647 HS_5193_A
c	596	16	1.1	516	100	AQ260464 AQ260464 CITBI-E1-
	597	16	1.1	516	103	AQ459533 AQ459533 HS_5085_A
c	598	16	1.1	516	104	AQ526174 AQ526174 HS_5312_B
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c	600	16	1.1	517	74	AV386565 AV386565
c	601	16	1.1	517	74	AV394940 AV394940
	602	16	1.1	518	34	AA464810 AA464810 zw63h03.r
c	603	16	1.1	519	102	AQ405413 AQ405413 HS_5045_B
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c	606	16	1.1	520	41	AI069876 AI069876 TENU2924
	607	16	1.1	520	74	AW172976 AW172976 xj23e12.x
c	608	16	1.1	521	36	AA625317 AA625317 af71d02.r
	609	16	1.1	521	38	AA539345 AA539345 LD17436.5
	610	16	1.1	521	46	AI399486 AI399486 NCSP6A6T7
	611	16	1.1	521	47	AI518349 AI518349 LD37835.5
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	613	16	1.1	523	47	AI542994 AI542994 SD09540.5
	614	16	1.1	523	90	AQ077612 AQ077612 CIT-HSP-2
	615	16	1.1	524	45	AI360257 AI360257 qy84g03.x
c	616	16	1.1	524	47	AI485718 AI485718 EST244039
	617	16	1.1	524	47	AI520534 AI520534 LD40723.5
c	618	16	1.1	524	62	AI902162 AI902162 618014H09
c	619	16	1.1	525	42	AU023596 AU023596 AU023596
	620	16	1.1	526	21	R11810 R11810 yf53a01.r1
	621	16	1.1	526	79	CNS00NEX AL081831 Arabidops
	622	16	1.1	527	74	AV386733 AV386733
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	624	16	1.1	528	36	AA607436 AA607436 vo41f12.r
c	625	16	1.1	528	37	AA651422 AA651422 31536 Lam
	626	16	1.1	528	46	AA965060 AA965060 UI-R-C0-h
c	627	16	1.1	528	64	AW017351 AW017351 EST272773
c	628	16	1.1	528	105	AQ647196 AQ647196 RPCI93-Dp
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c	630	16	1.1	530	47	AI485147 AI485147 EST243451
	631	16	1.1	530	88	AQ873935 AQ873935 V84A5 mTn
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	633	16	1.1	531	103	AQ493575 AQ493575 HS_5051_A
	634	16	1.1	532	40	AA953832 AA953832 oo38f08.s
c	635	16	1.1	533	64	AW034027 AW034027 EST277689
	636	16	1.1	533	74	AW205345 AW205345 UI-H-BI1-
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c	638	16	1.1	533	105	AQ653184 AQ653184 Sheared D
	639	16	1.1	534	31	AA314858 AA314858 EST186677
	640	16	1.1	534	42	AI085589 AI085589 oy68d11.x
	641	16	1.1	534	45	AI377819 AI377819 te58c09.x
c	642	16	1.1	534	46	AI436766 AI436766 th77d09.x
c	643	16	1.1	535	26	W30805 W30805 zb78b02.r1
	644	16	1.1	535	33	AA425119 AA425119 zv47c12.r
	645	16	1.1	535	39	AA897310 AA897310 al47c08.s
	646	16	1.1	536	38	AA391189 AA391189 LD09284.5
	647	16	1.1	536	45	AI356371 AI356371 qz21c07.x
c	648	16	1.1	537	70	AW146776 AW146776 614085A07
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	650	16	1.1	540	81	B68349 B68349 CIT-HSP-202
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	652	16	1.1	542	74	AV391117 AV391117 AV391117
	653	16	1.1	542	102	AQ357587 AQ357587 CITBI-E1-
	654	16	1.1	543	63	AI997339 AI997339 701553434
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	656	16	1.1	544	74	AJ273028 AJ273028 AJ273028
c	657	16	1.1	545	35	AA578929 AA578929 nf30c08.s
	658	16	1.1	545	102	AQ421972 AQ421972 RPCI-11-1
c	659	16	1.1	545	103	AQ505255 AQ505255 RPCI-11-3
	660	16	1.1	546	46	AI398952 AI398952 NCW06H8T7
	661	16	1.1	546	105	AQ664200 AQ664200 HS_5496_B
	662	16	1.1	547	34	AA495228 AA495228 fa01e11.r
c	663	16	1.1	547	74	AV390614 AV390614 AV390614
c	664	16	1.1	548	74	AV388006 AV388006
c	665	16	1.1	549	46	AI427284 AI427284 mc87d01.y
c	666	16	1.1	551	38	AA440626 AA440626 LD15467.5
c	667	16	1.1	551	50	AI673347 AI673347 tw35a01.x
	668	16	1.1	552	103	AQ458526 AQ458526 HS_5061_A
	669	16	1.1	553	44	AI294671 AI294671 LP08095.5
	670	16	1.1	554	44	AI255479 AI255479 ui86a10.x
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c	672	16	1.1	556	46	AI401887 AI401887 GH02955.3
c	673	16	1.1	558	34	AA533105 AA533105 nj19h04.s
	674	16	1.1	558	47	AI512956 AI512956 LD45123.5
	675	16	1.1	558	48	AI546628 AI546628 SD09441.5
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	677	16	1.1	558	90	AQ047197 AQ047197 RPCI11-35
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	687	16	1.1	568	100	AQ335251 AQ335251 HS_5014_B
c	688	16	1.1	569	74	AJ273352 AJ273352
	689	16	1.1	570	74	AV391088 AV391088
c	690	16	1.1	572	42	AI135047 AI135047 GH12661.5
	691	16	1.1	572	90	AQ063554 AQ063554 HS_2183_A
c	692	16	1.1	573	64	AW032970 AW032970 EST276529
c	693	16	1.1	574	47	AI512200 AI512200 LD43960.5
c	694	16	1.1	575	44	AI294207 AI294207 LP07528.5
	695	16	1.1	575	63	AI939408 AI939408 qy84g03.x
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	697	16	1.1	576	44	AI294573 AI294573 LP07978.5
	698	16	1.1	577	40	AA950599 AA950599 LD30457.5
	699	16	1.1	577	46	AA438472 AA438472 LD10361.5
	700	16	1.1	577	50	AI678875 AI678875 tu70c11.x
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	702	16	1.1	577	87	AQ757221 AQ757221 HS_5482_A
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	704	16	1.1	577	105	AQ623226 AQ623226 HS_5351_B
c	705	16	1.1	578	46	AI456712 AI456712 LD36828.5
c	706	16	1.1	578	47	AI489237 AI489237 EST247576
	707	16	1.1	578	51	AI711721 AI711721 605060F11
c	708	16	1.1	579	91	AQ162243 AQ162243 mgxb0012I
c	709	16	1.1	580	44	AI297207 AI297207 LP11463.5
	710	16	1.1	581	38	AA441011 AA441011 LD15755.5
	711	16	1.1	583	34	AA510274 AA510274 vh58d07.r
c	712	16	1.1	583	82	AQ694504 AQ694504 HS_5485_A
	713	16	1.1	584	28	AA116331 AA116331 mp97d09.r
	714	16	1.1	586	44	AI260647 AI260647 LP04595.5
	715	16	1.1	588	102	AQ365014 AQ365014 nbxb0062I
	716	16	1.1	589	47	AI514380 AI514380 LD40864.5
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	718	16	1.1	596	33	AA410754 AA410754 zv39b06.r
	719	16	1.1	596	47	AI543708 AI543708 SD10584.5
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c	721	16	1.1	599	87	AQ789461 AQ789461 HS_3171_A
c	722	16	1.1	600	25	N53467 N53467 yv41h09.s1
c	723	16	1.1	600	28	AA062231 AA062231 ml55g12.r
	724	16	1.1	600	44	AI257784 AI257784 LP06256.5
c	725	16	1.1	600	45	AI353076 AI353076 zeh0004.s
c	726	16	1.1	604	47	AI469386 AI469386 tm08b02.x
c	727	16	1.1	604	105	AQ640327 AQ640327 927P1-18D
	728	16	1.1	605	44	AI295658 AI295658 LP09348.5
c	729	16	1.1	606	59	AI780154 AI780154 EST261033
	730	16	1.1	606	90	AQ081462 AQ081462 CIT-HSP-2
	731	16	1.1	607	47	AI542212 AI542212 SD08360.5

	732	16	1.1	608	44	AI296164	AI296164 LP09993.5		805	16	1.1	699	74	AW179970	AW179970 MgA0022f
	733	16	1.1	610	36	AA611995	AA611995 vo94c10.r		806	16	1.1	700	74	AW179998	AW179998 MgA0052f
c	734	16	1.1	610	38	AA392637	AA392637 LD12870.5		807	16	1.1	702	51	AI731186	AI731186 BNLGHi885
	735	16	1.1	610	47	AI533343	AI533343 SD05122.5	c	808	16	1.1	706	42	AI110602	AI110602 HA0028 Hu
	736	16	1.1	610	63	AI977518	AI977518 EST272112	c	809	16	1.1	706	49	AF062710	AF062710 AF062710
c	737	16	1.1	610	70	AW157233	AW157233 au93b08.x		810	16	1.1	711	44	AI290800	AI290800 qm13c02.x
c	738	16	1.1	611	40	AA950861	AA950861 LD31012.5	c	811	16	1.1	711	105	AQ646949	AQ646949 RPCI93-Dp
	739	16	1.1	611	63	AI967120	AI967120 614006C03	c	812	16	1.1	717	99	AQ197771	AQ197771 CIT-HSP-2
	740	16	1.1	612	69	AV384344	AV384344 AV384344		813	16	1.1	718	33	AA392700	AA392700 LD11802.5
	741	16	1.1	613	61	AI833597	AI833597 605092F08	c	814	16	1.1	721	99	AQ254925	AQ254925 B15C22_T7
	742	16	1.1	613	63	AI980446	AI980446 pat.pk002		815	16	1.1	731	40	AA949701	AA949701 LD29683.5
	743	16	1.1	614	44	AI297651	AI297651 LP11996.5	c	816	16	1.1	732	45	AU006052	AU006052 AU006052
	744	16	1.1	614	47	AI519547	AI519547 LD39174.5		817	16	1.1	733	99	AQ254924	AQ254924 B838B18_T
	745	16	1.1	615	91	AQ158369	AQ158369 nbxb0011O	c	818	16	1.1	736	63	AI937005	AI937005 wp72a03.x
	746	16	1.1	617	34	AA536257	AA536257 LD16756.5		819	16	1.1	737	41	AF072312	AF072312 AF072312
	747	16	1.1	619	45	AI387441	AI387441 GH17970.5	c	820	16	1.1	740	88	AQ864513	AQ864513 nbeb0023M
	748	16	1.1	619	46	AI404321	AI404321 GH23975.5		821	16	1.1	744	47	AI523536	AI523536 th08a05.x
	749	16	1.1	620	30	AA246990	AA246990 LD06086.5		822	16	1.1	744	62	AI885857	AI885857 wl62e06.x
	750	16	1.1	620	39	AA827922	AA827922 od08h07.s	c	823	16	1.1	744	91	AQ160219	AQ160219 mgxb0003F
	751	16	1.1	620	105	AQ649892	AQ649892 Sheared D		824	16	1.1	745	30	AA246213	AA246213 LD06002.5
	752	16	1.1	621	44	AI295123	AI295123 LP08661.5		825	16	1.1	751	35	AA541083	AA541083 LD20873.5
	753	16	1.1	622	87	AQ809622	AQ809622 HS_4758_A	c	826	16	1.1	757	69	AU080671	AU080671 AU080671
	754	16	1.1	623	48	AI589770	AI589770 tm74b08.x		827	16	1.1	767	40	AA979310	AA979310 LD33801.5
	755	16	1.1	624	28	AA115293	AA115293 z108e10.r	c	828	16	1.1	767	81	B21887	B21887 F14M3-T7 IG
c	756	16	1.1	625	69	AW120122	AW120122 614085A07		829	16	1.1	768	40	AA978879	AA978879 LD33062.5
c	757	16	1.1	625	74	AW180908	AW180908 MgA0022r	c	830	16	1.1	772	51	AI747711	AI747711 ul21d02.x
c	758	16	1.1	626	44	AI257087	AI257087 LP05352.5		831	16	1.1	795	40	AA940888	AA940888 LD23209.5
	759	16	1.1	632	44	AI295392	AI295392 LP09007.5	c	832	16	1.1	796	46	AI440480	AI440480 tc88g03.x
c	760	16	1.1	634	47	AI486273	AI486273 EST244594		833	16	1.1	818	64	AW027041	AW027041 wt71d02.x
c	761	16	1.1	634	81	B87757	B87757 RPCI11-30F1		834	16	1.1	834	45	AI360239	AI360239 qy84e08.x
c	762	16	1.1	638	35	AA550252	AA550252 1374m3 gm	c	835	16	1.1	834	81	B01790	B01790 cSRL-140G1-
	763	16	1.1	638	91	AQ160965	AQ160965 nbxb0006C	c	836	16	1.1	841	38	AA264142	AA264142 LD07769.5
	764	16	1.1	639	44	AI294628	AI294628 LP08044.5		837	16	1.1	851	82	AQ741093	AQ741093 HS_2272_A
c	765	16	1.1	639	100	AQ279700	AQ279700 CITBI-E1-		838	16	1.1	854	51	AI762165	AI762165 wh90f07.x
	766	16	1.1	640	46	AI405479	AI405479 GH25488.5	c	839	16	1.1	856	82	AQ739429	AQ739429 HS_5387_B
c	767	16	1.1	640	74	AW180930	AW180930 MgA0052r	c	840	16	1.1	858	79	CNS0110I	AL099660 Drosophil
c	768	16	1.1	642	47	AI513498	AI513498 GH26616.5	c	841	16	1.1	861	82	AQ739069	AQ739069 HS_5387_B
	769	16	1.1	643	30	AA202648	AA202648 LD02818.5	c	842	16	1.1	865	81	B19627	B19627 T14B6-Sp6 T
	770	16	1.1	643	51	AI726042	AI726042 BNLGHi140		843	16	1.1	866	91	AQ161363	AQ161363 nbxb0006F
	771	16	1.1	646	79	AG008123	AG008123 Homo sapi	c	844	16	1.1	867	25	W08515	W08515 mb47h08.r1
	772	16	1.1	647	43	AI202117	AI202117 qi52b11.x		845	16	1.1	884	47	AI492655	AI492655 qz18c04.x
c	773	16	1.1	648	47	AI512603	AI512603 LD44522.5		846	16	1.1	885	79	CNS013VU	AL103380 Drosophil
c	774	16	1.1	649	41	AI055709	AI055709 coau0004N	c	847	16	1.1	908	39	AA896283	AA896283 vx62g12.r
	775	16	1.1	651	40	AA940757	AA940757 LD22973.5	c	848	16	1.1	915	79	CNS003R7	AL064863 Drosophil
c	776	16	1.1	651	63	AI999837	AI999837 614006C03		849	16	1.1	920	82	AQ688323	AQ688323 nbxb0077M
	777	16	1.1	652	44	AI295452	AI295452 LP09085.5	c	850	16	1.1	934	69	AU079146	AU079146 AU079146
	778	16	1.1	653	51	AI746161	AI746161 605081H04	c	851	16	1.1	988	79	CNS006FQ	AL064298 Drosophil
	779	16	1.1	654	61	AI833343	AI833343 605088B10		852	16	1.1	1031	26	W41746	W41746 mc63b07.r1
	780	16	1.1	656	51	AI743205	AI743205 wg89e07.x		853	16	1.1	1037	79	CNS00IOZ	AL075056 Drosophil
	781	16	1.1	658	37	AA695878	AA695878 GM04706.5		854	16	1.1	1049	79	CNS0054E	AL057622 Drosophil
	782	16	1.1	658	40	AA949140	AA949140 LD27922.5		855	16	1.1	1101	79	CNS000JV	AL058263 Drosophil
	783	16	1.1	663	62	AI894231	AI894231 md17c11.x		856	16	1.1	1101	79	CNS001B0	AL060149 Drosophil
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c	787	16	1.1	669	91	AQ157407	AQ157407 nbxb0009M	c	860	16	1.1	1201	79	CNS00ZZ2	AL098312 Drosophil
c	788	16	1.1	670	40	AA927510	AA927510 om70g11.s		861	15	1.1	31	62	AI916122	AI916122 wi47a09.x
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	790	16	1.1	674	46	AI438586	AI438586 486012B07		863	15	1.1	59	81	B44840	B44840 HS-1060-A1-
	791	16	1.1	675	91	AQ156170	AQ156170 nbxb0002J	c	864	15	1.1	79	34	AA525796	AA525796 ni61a08.s
c	792	16	1.1	677	90	AQ047841	AQ047841 cLM-3f2-t	c	865	15	1.1	93	80	AF009188	AF009188 Homo sapi
	793	16	1.1	677	105	AQ658119	AQ658119 Sheared D	c	866	15	1.1	106	33	AA416261	AA416261 vf38f12.r
c	794	16	1.1	678	105	AQ641663	AQ641663 RPCI93-Dp		867	15	1.1	120	38	AA750998	AA750998 ISMJ0135
	795	16	1.1	679	102	AQ413715	AQ413715 RPCI-11-1	c	868	15	1.1	124	30	AA219567	AA219567 zq99f10.s
c	796	16	1.1	680	100	AQ324990	AQ324990 mgxb0020M		869	15	1.1	134	32	AA371653	AA371653 EST83490
c	797	16	1.1	683	41	AI061971	AI061971 LD35083.5		870	15	1.1	139	38	AA790379	AA790379 vw05h08.r
c	798	16	1.1	683	105	AQ660590	AQ660590 Sheared D	c	871	15	1.1	140	25	N84764	N84764 J0812F Huma
	799	16	1.1	684	87	AQ780297	AQ780297 HS_3169_B	c	872	15	1.1	142	81	B22563	B22563 F15G6TR IGF
	800	16	1.1	687	69	AV383892	AV383892 AV383892	c	873	15	1.1	143	37	AA730270	AA730270 nz94b01.s
c	801	16	1.1	687	100	AQ274409	AQ274409 mgxb0015K		874	15	1.1	147	22	R29356	R29356 F1-477D 22
	802	16	1.1	688	37	AA735552	AA735552 LD21503.5	c	875	15	1.1	150	37	AA684852	AA684852 EST105576
c	803	16	1.1	692	99	AQ200219	AQ200219 RPCI11-45		876	15	1.1	150	48	AI618001	AI618001 zehn2431.
	804	16	1.1	699	44	AI290794	AI290794 qm13b05.x	c	877	15	1.1	151	49	AI664321	AI664321 ue84e09.r

878	15	1.1	151	60	AV128111	AV128111 AV128111
c 879	15	1.1	152	33	AA413420	AA413420 L794 Adul
c 880	15	1.1	153	70	AV247421	AV247421 AV247421
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c 885	15	1.1	166	62	AI929394	AI929394 au59h09.y
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915	15	1.1	205	28	AA119443	AA119443 mp67f03.r
c 916	15	1.1	205	42	AI157834	AI157834 ue59a10.r
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c 918	15	1.1	214	60	AV123450	AV123450 AV123450
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c 922	15	1.1	221	34	AA500360	AA500360 vg08e09.r
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924	15	1.1	222	36	AA640337	AA640337 nr21e06.s
925	15	1.1	222	71	AV257831	AV257831 AV257831
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929	15	1.1	225	33	AA396336	AA396336 vb46a02.r
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932	15	1.1	225	102	AQ415823	AQ415823 RPCI-11-1
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c 936	15	1.1	228	73	AV375804	AV375804 AV375804
937	15	1.1	229	50	AI707775	AI707775 as35c11.x
938	15	1.1	229	60	AV142070	AV142070 AV142070
c 939	15	1.1	229	73	AV365316	AV365316 AV365316
940	15	1.1	230	25	N60303	N60303 TgESTzy12c1
941	15	1.1	232	50	AV028596	AV028596 AV028596
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945	15	1.1	233	34	AA474779	AA474779 vd57g10.r
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948	15	1.1	234	26	W32367	W32367 zc66f06.r1
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953	15	1.1	235	70	AV241571	AV241571 AV241571
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956	15	1.1	236	47	AI518670	AI518670 LD38312.3
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968	15	1.1	241	49	AV021637	AV021637 AV021637
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971	15	1.1	241	72	AV289073	AV289073 AV289073
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976	15	1.1	244	51	AI713743	AI713743 UI-R-AG1-
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c 978	15	1.1	244	70	AV247006	AV247006 AV247006
979	15	1.1	245	20	T37102	T37102 EST102165 S
980	15	1.1	245	71	AV256272	AV256272 AV256272
981	15	1.1	245	72	AV331343	AV331343 AV331343
c 982	15	1.1	246	47	AI467479	AI467479 vd57g10.x
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c 984	15	1.1	247	48	AI612307	AI612307 486079B02
985	15	1.1	247	69	AW140154	AW140154 SWAMCAC42
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987	15	1.1	248	25	N56054	N56054 J6470F Huma
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c 990	15	1.1	249	51	AV055075	AV055075 AV055075
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992	15	1.1	249	73	AV343982	AV343982 AV343982
993	15	1.1	250	25	D79515	D79515 HUM272A09B
c 994	15	1.1	250	43	AI232607	AI232607 EST229295
995	15	1.1	250	59	AV089696	AV089696 AV089696
996	15	1.1	250	60	AV135645	AV135645 AV135645
997	15	1.1	250	61	AI824453	AI824453 tx70d11.x
c 998	15	1.1	250	69	AW115209	AW115209 rs62g10.y
c 999	15	1.1	251	37	AA731056	AA731056 nw50g08.s
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ALIGNMENTS

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RESULT   1
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LOCUS       C03492         200 bp    mRNA            EST       30-JUL-1996
DEFINITION  C03492 Human heart cDNA (YNakamura) Homo sapiens cDNA clone
            3NHC1609, mRNA sequence.
ACCESSION   C03492
VERSION     C03492.1  GI:1466743
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 200)
  AUTHORS   Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and
            Nakamura,Y.
  TITLE     Construction of a normalized directionally cloned cDNA library from
            adult heart and analysis of 3040 clones by partial sequencing
  JOURNAL   Genomics 35 (1), 231-235 (1996)
```

```
  MEDLINE   96299762
COMMENT     On Oct 18, 1995 this sequence version replaced gi:1023268.
            Contact: Yusuke Nakamura
            Institute of Medical Science
            University of Tokyo
            4-6-1, Shirokanedai, Minato-ku, Tokyo 108,  Japan
            Tel: 81-3-5449-5372
            Fax: 81-3-5449-5433
            Email: yusuke@ims.u-tokyo.ac.jp.
FEATURES              Location/Qualifiers
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                      /dev_stage="adult"
                      /note="Organ: heart; normalized directionally cloned cDNA
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ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 6.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     817 ggcatctcctttgccatccc 836
           ||||||||||||||||||||
Db     123 GGCATCTCCTTTGCCATCCC 142


RESULT   2
AA958603
LOCUS       AA958603      304 bp    mRNA            EST       08-MAY-1998
DEFINITION  ua15e07.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone
            IMAGE:1346820 5' similar to TR:Q92743 Q92743 NOVEL SERINE PROTEASE.
            ;, mRNA sequence.
ACCESSION   AA958603
VERSION     AA958603.1  GI:3124833
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 19, 1998 this sequence version replaced gi:2282401.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:695612
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
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                      /sex="male"
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                      /dev_stage="4 weeks"
                      /lab_host="DH10B"
                      /note="Organ: mammary gland; Vector: pT7T3D-Pac
                      (Pharmacia) with a modified polylinker; Site_1: Not I;
                      Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                      oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCGAATGGTTTTTTTTTTTTTTTTTTTTT
                      T 3']; double-stranded cDNA was ligated to Eco RI
                      adaptors (Pharmacia), digested with Not I and cloned into
                      the Not I and Eco RI sites of the modified pT7T3 vector.
                      RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
                      constructed and normalized by Bento Soares and M.Fatima
                      Bonaldo."
BASE COUNT       68 a     95 c     80 g     61 t
ORIGIN


  Query Match             1.4%;  Score 20;  DB 40;  Length 304;
  Best Local Similarity   100.0%;  Pred. No. 6.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     817 ggcatctcctttgccatccc 836
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Db     239 GGCATCTCCTTTGCCATCCC 258


RESULT   3
AI324092
LOCUS       AI324092      329 bp    mRNA            EST       23-DEC-1998
DEFINITION  mh04b12.x1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA
            clone IMAGE:441503 3' similar to TR:Q92743 Q92743 NOVEL SERINE
            PROTEASE. ;, mRNA sequence.
ACCESSION   AI324092
VERSION     AI324092.1  GI:4058521
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044727.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:266839
            This clone was previously sequenced on the 5' end only, this new
            data is from the 3' end
            Possible reversed clone: similarity on wrong strand
            Possible reversed clone: polyT not found
            High quality sequence stop: 325.
FEATURES              Location/Qualifiers
     source           1. .329
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:441503"
                      /clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
```

```
                     /sex="unknown"
                     /tissue_type="placenta"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAATTTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT       70 a     99 c     93 g     67 t
ORIGIN


  Query Match             1.4%;  Score 20;  DB 44;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 6.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    817 ggcatctcctttgccatccc 836
          ||||||||||||||||||||
Db    239 GGCATCTCCTTTGCCATCCC 258


RESULT   4
AA475998
LOCUS       AA475998      445 bp    mRNA            EST       18-JUN-1997
DEFINITION  vh25h10.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone
            IMAGE:876547 5', mRNA sequence.
ACCESSION   AA475998
VERSION     AA475998.1  GI:2203849
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 445)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Nov 29, 1993 this sequence version replaced gi:430468.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:516027
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 437.
FEATURES             Location/Qualifiers
     source          1. .445
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:876547"
                     /clone_lib="Soares mouse mammary gland NbMMG"
                     /sex="male"
                     /tissue_type="mammary gland"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /note="Organ: mammary gland; Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGAATGGTTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
                     constructed and normalized by Bento Soares and M.Fatima
                     Bonaldo."
BASE COUNT      103 a    140 c    111 g     91 t
ORIGIN


  Query Match             1.4%;  Score 20;  DB 34;  Length 445;
  Best Local Similarity   100.0%;  Pred. No. 7.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    817 ggcatctcctttgccatccc 836
          ||||||||||||||||||||
Db     73 GGCATCTCCTTTGCCATCCC 92


RESULT   5
AA013893/c
LOCUS       AA013893      458 bp    mRNA            EST       21-JAN-1997
DEFINITION  mh04b12.r1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA
            clone IMAGE:441503 5' similar to SW:HTOA_HAEIN P45129 PROBABLE
            PERIPLASMIC SERINE PROTEASE DO/HHOA-LIKE PRECURSOR. [1] ;, mRNA
            sequence.
ACCESSION   AA013893
VERSION     AA013893.1  GI:1474919
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 458)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On May 5, 1995 this sequence version replaced gi:797824.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:266839
            Possible reversed clone: similarity on wrong strand
            Seq primer: ETPrimer
            High quality sequence stop: 355.
FEATURES             Location/Qualifiers
     source          1. .458
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:441503"
                     /clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
                     /sex="unknown"
                     /tissue_type="placenta"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'
```

TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAATTTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 94 a 119 c 129 g 116 t
ORIGIN

Query Match 1.4%; Score 20; DB 27; Length 458;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 817 ggcatctcctttgccatccc 836
||||||||||||||||||||
Db 328 GGCATCTCCTTTGCCATCCC 309

RESULT 6
AA447906
LOCUS AA447906 482 bp mRNA EST 04-JUN-1997
DEFINITION zx11b06.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:786131 5' similar to TR:G473503 G473503 ;, mRNA sequence.
ACCESSION AA447906
VERSION AA447906.1 GI:2161576
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 482)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1318534.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham.
FEATURES Location/Qualifiers
source 1. .482
/organism="Homo sapiens"
/db_xref="GDB:5983750"
/db_xref="taxon:9606"
/clone="IMAGE:786131"
/clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGGCCGCTTAATTTTTTTTTTTTTTTT 3']
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 110 a 141 c 142 g 89 t
ORIGIN

Query Match 1.4%; Score 20; DB 33; Length 482;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 817 ggcatctcctttgccatccc 836
||||||||||||||||||||
Db 261 GGCATCTCCTTTGCCATCCC 280

RESULT 7
AI322461/c
LOCUS AI322461 557 bp mRNA EST 23-DEC-1998
DEFINITION mh04b12.y1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA
clone IMAGE:441503 5' similar to TR:Q92743 Q92743 NOVEL SERINE
PROTEASE. ;, mRNA sequence.
ACCESSION AI322461
VERSION AI322461.1 GI:4056890
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 557)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT On Jan 14, 1998 this sequence version replaced gi:1877700.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:266839
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 430.
FEATURES Location/Qualifiers
source 1. .557
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:441503"
/clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
/sex="unknown"
/tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5'
TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAATTTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 114 a 154 c 159 g 130 t
ORIGIN

Query Match 1.4%; Score 20; DB 44; Length 557;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    817 ggcatctcctttgccatccc 836
          ||||||||||||||||||||
Db    330 GGCATCTCCTTTGCCATCCC 311


RESULT   8
AA672965/c
LOCUS       AA672965      354 bp    mRNA            EST       26-NOV-1997
DEFINITION  vn48b11.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
            IMAGE:1024413 5', mRNA sequence.
ACCESSION   AA672965
VERSION     AA672965.1  GI:2646247
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 354)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1393485.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:575189
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 342.
FEATURES             Location/Qualifiers
     source          1. .354
                     /organism="Mus musculus"
                     /strain="C3H"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1024413"
                     /clone_lib="Barstead mouse myotubes MPLRB5"
                     /cell_line="C2C12"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACGAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     [AATTCGGATCCTTG], digested with Not I and cloned into the
                     Not I and Eco RI sites of the modified pT7T3 vector.
                     Library constructed by Bob Barstead. The C2C12 cell line
                     (available from ATCC, catalog # CRL-1772) differentiates
                     rapidly, forming contractile myotubes and producing
                     characteristic muscle proteins. "
BASE COUNT       50 a    124 c    124 g     56 t
ORIGIN


  Query Match             1.4%;  Score 19;  DB 37;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    217 gcagcccccgccccgcgca 235
          ||||||||||||||||||||
Db     74 GCAGCCCCCGCCCCGCGCA 56


RESULT   9
AI538510
LOCUS       AI538510      508 bp    mRNA            EST       13-APR-1999
DEFINITION  td07e06.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2074978 3'
            similar to contains MSR1.t1 MSR1 repetitive element ;, mRNA
            sequence.
ACCESSION   AI538510
VERSION     AI538510.1  GI:4452645
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jun 5, 1998 this sequence version replaced gi:3188259.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
            M.D., Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Insert Length: 817   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 487.
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2074978"
                     /clone_lib="NCI_CGAP_CLL1"
                     /tissue_type="B-cell, chronic lymphotic leukemia"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTGCTTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     Library is normalized, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT       81 a    182 c    129 g    115 t      1 others
ORIGIN


  Query Match             1.4%;  Score 19;  DB 47;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    212 ttcaggcagcccccgcccc 230
          ||||||||||||||||||||
Db    191 TTCAGGCAGCCCCCGCCCC 209


RESULT  10
AA106132/c
LOCUS       AA106132      633 bp    mRNA            EST       04-FEB-1997
DEFINITION  mm20f05.r1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA
            clone IMAGE:522081 5' similar to SW:SX14_MOUSE Q04892 SOX-14
            PROTEIN ;, mRNA sequence.
ACCESSION   AA106132
VERSION     AA106132.1  GI:1656164
KEYWORDS    EST.
SOURCE      house mouse.
```

```
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 633)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1315910.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:315929
            Possible reversed clone: similarity on wrong strand
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 374.
FEATURES             Location/Qualifiers
     source          1. .633
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:522081"
                     /clone_lib="Stratagene mouse diaphragm (#937303)"
                     /tissue_type="diaphragm"
                     /dev_stage="adult"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: diaphragm; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA
                     prepared from diaphragm muscle.  Primer: Oligo dT. Average
                     insert size: 1.5 kb. Uni-ZAP XR Vector; ~5' adaptor
                     sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
                     CTCGAGTTTTTTTTTTTTTTTTT 3'"
BASE COUNT      131 a    191 c    221 g     85 t      5 others
ORIGIN


  Query Match             1.4%;  Score 19;  DB 28;  Length 633;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    217 gcagcccccgccccgcgca 235
          ||||||||||||||||||||
Db     49 GCAGCCCCCGCCCCGCGCA 31


RESULT  11
AI756231
LOCUS       AI756231       63 bp    mRNA            EST       23-JUN-1999
DEFINITION  ea41d11.y1 Eimeria S5-2 Sporozoite stage Eimeria tenella cDNA 5'
            similar to SW:YNQ3_YEAST P53893 HYPOTHETICAL 124.5 KD PROTEIN IN
            SKO1-RPL44A INTERGENIC REGION. [1] ;, mRNA sequence.
ACCESSION   AI756231
VERSION     AI756231.1  GI:5149954
KEYWORDS    EST.
SOURCE      Eimeria tenella.
  ORGANISM  Eimeria tenella
            Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
            Eimeria.
REFERENCE   1  (bases 1 to 63)
  AUTHORS   Liberator,P., Diaz,C., Tang,K., Marra,M., Hillier,L., Kucaba,T.,
            Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B.,
            Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D.,
            Harvey,N., Schurk,R., Ritter,E., Kohn,S., Florence,N., Shin,T.,
            Jackson,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R. and
            Sibley,D.
  TITLE     WashU-Merck Eimeria tenella project
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948270.
            Contact: David Sibley, Ph.D.
            WashU-Merck Eimeria tenella project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Contact David Sibley (toxoest@borcim.wustl.edu) for further
            information relating to organism, libraries, or clone availability.

            Possible reversed clone: similarity on wrong strand
            Seq primer: -40RP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .63
                     /organism="Eimeria tenella"
                     /strain="LS18"
                     /db_xref="taxon:5802"
                     /clone_lib="Eimeria S5-2 Sporozoite stage"
                     /dev_stage="Sporozoite"
                     /lab_host="SOLR E. coli"
                     /note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; Sporozoites were obtained from in vitro sporulated
                     and excysted oocysts of E. tenella grown in chickens.
                     cDNA was synthesized from poly mRNA using an oligo-dT
                     primer containing a XhoI site. Following second strand
                     synthesis, EcoRI adapters were ligated to  the cDNA and
                     products were size-selected on Sephacryl S500.  cDNAs were
                     digested with EcoRI/XhoI and cloned into lambda Zap II
                     (Stratagene).  Clones were converted to phagemids by mass
                     excision  using ExAssist helper phage and SOLR cells
                     (Stratagene ).  Insert  sizes range from 1.2-2.9 kb."
BASE COUNT      21 a     16 c     12 g     14 t
ORIGIN


  Query Match             1.3%;  Score 18;  DB 51;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 67;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1148 aaatcacaatcaaagcca 1165
           ||||||||||||||||||
Db     18 AAATCACAATCAAAGCCA 35


RESULT  12
D37319
LOCUS       D37319         330 bp    mRNA            EST       24-OCT-1994
DEFINITION  CELK043HXF Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
            clone yk43h10 5', mRNA sequence.
ACCESSION   D37319
VERSION     D37319.1  GI:525710
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans.
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
            Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 330)
  AUTHORS   Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
            Tabara,H.
  TITLE     Toward an expression map of the C.elegans genome
  JOURNAL   Unpublished (1994)
COMMENT     Contact: Yuji Kohara
            Gene Library Lab
            National Institute of Genetics
            Yata 1111, Mishima, Shizuoka 411, Japan
            Tel: 81-559-81-6854
            Fax: 81-559-81-6855
            Email: ykohara@lab.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .330
```

```
                     /organism="Caenorhabditis elegans"
                     /strain="CB1489 him-8(e1489)"
                     /db_xref="taxon:6239"
                     /clone="yk43h10"
                     /clone_lib="Yuji Kohara unpublished cDNA"
                     /sex="hermaphrodite, male"
                     /tissue_type="whole animal"
                     /dev_stage="varied"
BASE COUNT       125 a     56 c     54 g     95 t
ORIGIN


  Query Match             1.3%;  Score 18;  DB 20;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    295 ttctacgaatttttcaaa 312
          ||||||||||||||||||
Db     76 TTCTACGAATTTTTCAAA 93


RESULT  13
D68430
LOCUS       D68430        360 bp    mRNA            EST       07-DEC-1995
DEFINITION  CELK131C4F Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
            clone yk131c4 5', mRNA sequence.
ACCESSION   D68430
VERSION     D68430.1  GI:1107152
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans.
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
            Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 360)
  AUTHORS   Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
            Tabara,H.
  TITLE     Toward an expression map of the C.elegans genome
  JOURNAL   Unpublished (1994)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:785236.
            Contact: Yuji Kohara
            Gene Library Lab
            National Institute of Genetics
            Yata 1111, Mishima, Shizuoka 411, Japan
            Tel: 81-559-81-6854
            Fax: 81-559-81-6855
            Email: ykohara@lab.nig.ac.jp
            Insert Length: 404   Std Error: 0.00
            High quality sequence stop: 193.
FEATURES             Location/Qualifiers
     source          1. .360
                     /organism="Caenorhabditis elegans"
                     /strain="CB1489 him-8(e1489)"
                     /db_xref="taxon:6239"
                     /clone="yk131c4"
                     /clone_lib="Yuji Kohara unpublished cDNA"
                     /sex="hermaphrodite, male"
                     /tissue_type="whole animal"
                     /dev_stage="varied"
BASE COUNT       134 a     65 c     60 g    101 t
ORIGIN


  Query Match             1.3%;  Score 18;  DB 24;  Length 360;
  Best Local Similarity   100.0%;  Pred. No. 84;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    295 ttctacgaatttttcaaa 312
          ||||||||||||||||||
Db    128 TTCTACGAATTTTTCAAA 145


RESULT  14
AI585708
LOCUS       AI585708      371 bp    mRNA            EST       06-APR-1999
DEFINITION  mq93b02.y1 Stratagene mouse heart (#937316) Mus musculus cDNA clone
            IMAGE:586251 5' similar to TR:Q15290 Q15290 RB PROTEIN BINDING
            PROTEIN. ;, mRNA sequence.
ACCESSION   AI585708
VERSION     AI585708.1  GI:4571605
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 371)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 5, 1998 this sequence version replaced gi:3187526.
            Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            This read is a RESEQUENCE of a previously sequenced mouse clone
            This read has been verified (found to hit its original self in the
            correct orientation)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 337.
FEATURES             Location/Qualifiers
     source          1. .371
                     /organism="Mus musculus"
                     /strain="NIH/Swiss"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:586251"
                     /clone_lib="Stratagene mouse heart (#937316)"
                     /sex="pooled"
                     /tissue_type="heart"
                     /dev_stage="13 day embryos"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: heart; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. 93 pooled NIH/Swiss 13 day embryo hearts.
                     Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
                     adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor
                     sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
BASE COUNT       103 a     121 c     56 g     91 t
ORIGIN


  Query Match             1.3%;  Score 18;  DB 48;  Length 371;
  Best Local Similarity   100.0%;  Pred. No. 85;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1030 gacatcgtcctcagcctc 1047
          ||||||||||||||||||
Db    252 GACATCGTCCTCAGCCTC 269


RESULT  15
AA140161
LOCUS       AA140161      420 bp    mRNA            EST       11-FEB-1997
DEFINITION  mq93b02.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone
            IMAGE:586251 5' similar to TR:G755748 G755748 RB PROTEIN BINDING
            PROTEIN. ;, mRNA sequence.
ACCESSION   AA140161
VERSION     AA140161.1  GI:1702364
KEYWORDS    EST.
SOURCE      house mouse.
```

```
   ORGANISM  Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  REFERENCE  1  (bases 1 to 420)
    AUTHORS  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
             Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
             Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
             Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
             Waterston,R.
    TITLE    The WashU-HHMI Mouse EST Project
  JOURNAL    Unpublished (1996)
  COMMENT    On Sep 12, 1996 this sequence version replaced gi:1407398.
             Contact: Marra M/Mouse EST Project
             WashU-HHMI Mouse EST Project
             Washington University School of MedicineP
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: mouseest@watson.wustl.edu
             This clone is available royalty-free through LLNL ; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
             MGI:360899
             Seq primer: -28m13 rev1 ET from Amersham
             High quality sequence stop: 380.
  FEATURES             Location/Qualifiers
       source          1. .420
                       /organism="Mus musculus"
                       /strain="NIH/Swiss"
                       /db_xref="taxon:10090"
                       /clone="IMAGE:586251"
                       /clone_lib="Stratagene mouse heart (#937316)"
                       /sex="pooled"
                       /tissue_type="heart"
                       /dev_stage="13 day embryos"
                       /lab_host="SOLR (kanamycin resistant)"
                       /note="Organ: heart; Vector: pBluescript SK-; Site_1:
                       EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                       Oligo dT. 93 pooled NIH/Swiss 13 day embryo hearts.
                       Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
                       adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor
                       sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
  BASE COUNT      121 a    131 c     65 g    103 t
  ORIGIN


    Query Match             1.3%;  Score 18;  DB 29;  Length 420;
    Best Local Similarity   100.0%;  Pred. No. 86;
    Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

  Qy   1030 gacatcgtcctcagcctc 1047
            ||||||||||||||||||
  Db    251 GACATCGTCCTCAGCCTC 268


  Search completed: April 14, 2000, 17:43:40
  Job time: 7274 sec
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